Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802049	BAN102312	39%	90.3%	92.4%
SAU802049	BAN108913	63%	98.5%	98.3%
SAU802049	BAN103034	63%	98.5%	100%
SAU802049	BFR100429	40%	96.8%	99.1%
SAU802049	BPT100362	42%	95.9%	86.6%
SAU802049	BBU100768	42%	96.2%	94.2%
SAU802049	BCE114776	43%	78.9%	86.2%
SAU802049	BFU102589	45%	91.5%	88.7%
SAU802049	BMA105419	44%	90.6%	88.0%
SAU802049	CJU101268	36%	93.8%	94.6%
SAU802049	CPN200562	40%	92.4%	92.4%
SAU802049	CTR200463	43%	91.8%	92.6%
SAU802049	CAC103068	52%	98.8%	99.7%
SAU802049	CBO100390	55%	98.8%	99.7%
SAU802049	CDF101563	53%	97.9%	96.6%
SAU802049	CDP100064	45%	92.7%	93.1%
SAU802049	EBC100417	42%	94.4%	96.1%
SAU802049	EFA200289	58%	98.5%	97.1%
SAU802049	EFM201462	58%	97.4%	98.8%
SAU802049	ECO102998	41%	97.9%	99.1%
SAU802049	HIN100509	44%	94.4%	95.6%
SAU802049	HPY101561	34%	93.8%	95.6%
SAU802049	KPN306799	37%	54.8%	97.9%
SAU802049	LPN103299	43%	83.6%	92.2%
SAU802049	LMO102931	59%	98.8%	98.5%
SAU802049	MCA101243	40%	94.1%	94.5%
SAU802049	MAV102882	48%	51.9%	97.3%
SAU802049	MBV101140	44%	92.1%	92.7%
SAU802049	MLP100243	44%	91.2%	90.3%
SAU802049	MTU203373	44%	92.1%	92.7%
SAU802049	MGE100046	33%	97.4%	100%
SAU802049	MPN100095	36%	97.4%	100%
SAU802049	NGO101700	40%	93.0%	94.9%
SAU802049	NME200611	39%	93.0%	94.9%
SAU802049	PMU101238	43%	97.9%	98.8%
SAU802049	PRT100528	41%	97.9%	98.2%
SAU802049	PAE200579	44%	90.0%	91.2%
SAU802049	PPU107523	45%	97.7%	98.8%
SAU802049	PSY103381	43%	98.2%	99.4%
SAU802049	SPA101473	35%	62.5%	89.4%
SAU802049	STY100806	41%	97.9%	99.1%
SAU802049	SAU802049	100%	100%	100%
SAU802049	SEP201284	80%	99.4%	98.3%
SAU802049	SHA101340	78%	100%	100%
SAU802049	SMU100718	53%	97.7%	98.5%
SAU802049	SPN400131	55%	97.1%	97.9%
SAU802049	SPY201441	53%	98.2%	97.4%
SAU802049	TPA100672	40%	92.1%	89.2%
SAU802049	UUR100415	37%	92.7%	96.6%
SAU802049	YPS001964	43%	90.0%	91.1%
SAU802054	ABA105924	43%	94.1%	98.4%
SAU802054	BAN113044	53%	93.0%	99.8%
SAU802054	BAN109521	54%	95.8%	99.5%
SAU802054	BFR10273	41%	89.1%	99.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802054	BPT102555	42%	93.5%	98.2%
SAU802054	BCE111312	45%	93.4%	89.3%
SAU802054	BFU106339	44%	93.4%	95.1%
SAU802054	BMA108273	44%	93.4%	95.1%
SAU802054	CJU100535	44%	93.5%	97.7%
SAU802054	CAC100732	43%	93.5%	98.7%
SAU802054	CDF100458	43%	92.0%	97.3%
SAU802054	CDP100196	42%	93.7%	86.2%
SAU802054	EBC103122	42%	93.5%	99.3%
SAU802054	ECO100077	42%	94.1%	93.5%
SAU802054	HIN101552	43%	93.5%	97.6%
SAU802054	KPN302040	42%	93.5%	98.9%
SAU802054	LPN103264	22%	83.2%	83.5%
SAU802054	LMO101325	59%	96.6%	99.7%
SAU802054	MCA100916	43%	95.9%	94.6%
SAU802054	MAV101431	43%	93.7%	90.5%
SAU802054	MBV101317	43%	93.7%	91.1%
SAU802054	MLP101038	43%	95.1%	91.4%
SAU802054	MTU202965	43%	93.7%	91.1%
SAU802054	NGO101351	43%	93.5%	97.4%
SAU802054	NME201625	43%	93.5%	97.4%
SAU802054	PMU100870	43%	93.5%	97.6%
SAU802054	PRT105730	42%	93.5%	98.9%
SAU802054	PAE204692	41%	92.4%	96.7%
SAU802054	PPU111169	43%	87.3%	98.5%
SAU802054	PSY104459	41%	84.7%	98.3%
SAU802054	SPA102770	42%	93.5%	98.9%
SAU802054	STY102149	42%	93.5%	98.9%
SAU802054	STM101000	42%	93.5%	98.9%
SAU802054	SAU802054	100%	100%	100%
SAU802054	SEP201291	81%	94.1%	95.0%
SAU802054	SHA101346	79%	94.7%	94.4%
SAU802054	SMU101464	56%	94.9%	98.4%
SAU802054	SPN400401	54%	95.1%	98.6%
SAU802054	VCH102447	43%	94.1%	98.4%
SAU802054	YPS000964	41%	94.1%	98.4%
SAU802055	ABA105739	28%	88.1%	44.8%
SAU802055	BAN101552	40%	88.1%	43.8%
SAU802055	BFR103117	33%	67.9%	30.1%
SAU802055	BPT102556	24%	88.1%	44.8%
SAU802055	BCE113712	30%	96.4%	44.6%
SAU802055	BFU106342	31%	88.1%	44.8%
SAU802055	BMA102494	30%	96.4%	47.9%
SAU802055	CJU100536	28%	98.8%	53.9%
SAU802055	EBC101943	33%	88.1%	44.8%
SAU802055	ECO100078	32%	88.1%	44.8%
SAU802055	HIN101551	28%	88.1%	44.8%
SAU802055	KPN301558	31%	88.1%	42.2%
SAU802055	LMO101469	36%	97.6%	49.1%
SAU802055	MCA100917	26%	85.7%	39.4%
SAU802055	MAV101430	34%	86.9%	42.9%
SAU802055	MBV101315	34%	86.9%	42.9%
SAU802055	MTU202964	34%	86.9%	42.9%
SAU802055	NGO101348	29%	88.1%	44.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802055	NME201624	29%	88.1%	44.8%
SAU802055	PMU100869	27%	88.1%	44.8%
SAU802055	PAE204691	27%	96.4%	46.0%
SAU802055	PPU100092	28%	96.4%	46.0%
SAU802055	PSY104460	27%	96.4%	46.0%
SAU802055	SPA102565	32%	88.1%	83.9%
SAU802055	STY103145	32%	88.1%	44.5%
SAU802055	STM102857	32%	88.1%	44.8%
SAU802055	SAU802055	100%	100%	100%
SAU802055	SEP204150	61%	89.3%	97.4%
SAU802055	SHA102434	62%	89.3%	93.8%
SAU802055	SMU101466	32%	96.4%	49.4%
SAU802055	SPN400402	30%	96.4%	47.6%
SAU802055	VCH102446	30%	89.3%	45.1%
SAU802055	YPS000965	31%	85.7%	43.3%
SAU802056	ABA105073	53%	98.5%	97.6%
SAU802056	BAN104049	60%	97.3%	99.7%
SAU802056	BAN109399	66%	98.8%	98.2%
SAU802056	BFR11737	36%	84.4%	82.4%
SAU802056	BPT102557	54%	98.5%	97.6%
SAU802056	BCE101787	57%	99.1%	98.5%
SAU802056	BFU106345	57%	99.1%	98.5%
SAU802056	BMA102817	57%	99.1%	98.5%
SAU802056	CJU100593	59%	98.8%	97.4%
SAU802056	CAC103323	56%	97.0%	96.4%
SAU802056	CDF103947	61%	98.2%	99.4%
SAU802056	CDP100202	58%	97.0%	96.4%
SAU802056	EBC102901	33%	94.0%	91.9%
SAU802056	EFM100577	60%	30.8%	98.1%
SAU802056	ECO103688	33%	94.0%	91.9%
SAU802056	HIN100663	31%	94.0%	91.9%
SAU802056	HPY100326	43%	95.2%	96.7%
SAU802056	KPN302041	33%	94.0%	91.9%
SAU802056	LMO100212	77%	98.2%	99.1%
SAU802056	MCA100918	54%	98.5%	97.1%
SAU802056	MAV101429	56%	97.0%	97.6%
SAU802056	MBV101313	56%	97.0%	97.6%
SAU802056	MLP101036	54%	98.8%	99.4%
SAU802056	MTU202963	56%	97.0%	97.6%
SAU802056	NGO101342	56%	98.5%	97.6%
SAU802056	NME201622	56%	98.5%	97.6%
SAU802056	PMU101284	32%	95.2%	92.9%
SAU802056	PRT103939	31%	95.2%	92.7%
SAU802056	PAE204690	56%	98.5%	97.6%
SAU802056	PPU100091	55%	98.5%	97.6%
SAU802056	PSY104461	55%	98.5%	97.6%
SAU802056	SPA103746	31%	62.3%	94.9%
SAU802056	STY102126	33%	94.0%	91.9%
SAU802056	STM101019	33%	94.0%	91.9%
SAU802056	SAU802056	100%	100%	100%
SAU802056	SEP201300	89%	100%	100%
SAU802056	SHA101347	88%	100%	100%
SAU802056	SMU101468	67%	96.4%	94.7%
SAU802056	SPN400403	68%	96.4%	94.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802056	VCH100160	30%	95.2%	92.7%
SAU802056	YPS001623	32%	94.0%	91.9%
SAU802059	ABA104781	55%	98.9%	99.2%
SAU802059	BAN100313	64%	98.9%	100%
SAU802059	BAN100367	66%	99.3%	97.8%
SAU802059	BFR12153	48%	99.1%	99.6%
SAU802059	BPT101910	54%	99.1%	97.3%
SAU802059	BCE108881	54%	99.6%	99.8%
SAU802059	BFU100662	55%	98.5%	91.7%
SAU802059	BMA104026	54%	99.1%	61.9%
SAU802059	CJU101621	56%	99.3%	98.7%
SAU802059	CAC102015	36%	99.1%	98.8%
SAU802059	CDF100900	33%	99.8%	100%
SAU802059	CDP100261	54%	97.1%	94.8%
SAU802059	EBC102532	55%	99.6%	100%
SAU802059	ECO100072	54%	99.6%	99.8%
SAU802059	HIN100969	54%	100%	99.8%
SAU802059	HPY100766	25%	75.2%	40.9%
SAU802059	KPN301553	54%	99.6%	99.8%
SAU802059	LMO100765	75%	100%	98.9%
SAU802059	MCA100223	54%	98.9%	99.2%
SAU802059	MAV108159	54%	97.4%	95.8%
SAU802059	MBV102077	52%	97.4%	96.4%
SAU802059	MLP101031	54%	97.8%	95.3%
SAU802059	MTU202950	52%	97.4%	96.4%
SAU802059	NGO101165	54%	98.7%	98.7%
SAU802059	NME201321	54%	98.7%	98.7%
SAU802059	PMU101960	54%	99.6%	99.4%
SAU802059	PRT101170	56%	99.1%	98.7%
SAU802059	PAE203119	55%	99.6%	99.4%
SAU802059	PPU103214	55%	99.6%	98.5%
SAU802059	PSY104878	55%	99.3%	98.7%
SAU802059	SPA102560	54%	97.4%	100%
SAU802059	STY103139	54%	99.6%	99.8%
SAU802059	STM104156	45%	99.3%	98.5%
SAU802059	SAU802059	100%	100%	100%
SAU802059	SEP201303	89%	100%	100%
SAU802059	SHA102193	80%	59.9%	100%
SAU802059	SMU100436	65%	99.3%	98.5%
SAU802059	VCH102456	55%	98.9%	98.9%
SAU802059	YPS000958	55%	99.1%	97.3%
SAU802063	ABA100497	40%	98.7%	90.4%
SAU802063	BAN103890	51%	97.2%	98.3%
SAU802063	BAN110897	57%	99.4%	99.2%
SAU802063	BFR10814	49%	35.3%	87.7%
SAU802063	BFR10451	47%	97.1%	97.5%
SAU802063	BPT101858	42%	96.8%	89.3%
SAU802063	BCE100683	42%	98.9%	88.0%
SAU802063	BFU102354	43%	98.9%	91.8%
SAU802063	BMA107964	43%	98.9%	87.3%
SAU802063	CAC102993	53%	98.2%	98.7%
SAU802063	CBO101100	50%	98.6%	98.8%
SAU802063	CDF101569	52%	98.6%	99.0%
SAU802063	CDP101150	43%	98.3%	92.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802063	EBC103842	42%	99.3%	92.5%
SAU802063	EFA200142	56%	99.2%	98.4%
SAU802063	EFM202462	56%	99.7%	99.2%
SAU802063	ECO103330	42%	94.8%	92.7%
SAU802063	HIN100547	42%	99.3%	94.4%
SAU802063	KPN300029	38%	25.3%	96.1%
SAU802063	KPN307162	42%	99.3%	92.5%
SAU802063	LPN100520	41%	98.2%	89.6%
SAU802063	LMO101697	57%	99.9%	99.0%
SAU802063	MCA100121	39%	99.3%	88.6%
SAU802063	NGO101872	42%	96.8%	91.4%
SAU802063	NME200185	42%	96.8%	91.4%
SAU802063	PMU101448	42%	99.3%	90.9%
SAU802063	PRT102821	42%	99.3%	92.4%
SAU802063	PAE205196	42%	96.9%	90.0%
SAU802063	PPU110008	42%	98.6%	92.2%
SAU802063	PSY103044	42%	98.6%	92.4%
SAU802063	SPA103543	41%	98.2%	99.9%
SAU802063	STY101364	42%	99.3%	92.5%
SAU802063	STM102920	42%	99.3%	92.6%
SAU802063	SAU802063	100%	100%	100%
SAU802063	SEP201321	76%	100%	100%
SAU802063	SHA100107	86%	42.7%	100%
SAU802063	SMU100019	49%	99.6%	99.6%
SAU802063	SPN400808	51%	97.6%	96.6%
SAU802063	SPY200418	49%	100%	99.7%
SAU802063	TPA100914	42%	99.2%	90.0%
SAU802063	UUR100027	41%	99.3%	99.7%
SAU802063	VCH102678	42%	99.3%	93.0%
SAU802063	YPS001556	41%	99.3%	90.8%
SAU802070	ABA104714	34%	93.5%	98.0%
SAU802070	BAN108606	28%	74.1%	73.6%
SAU802070	BAN113034	40%	95.3%	94.6%
SAU802070	BFR100168	31%	94.0%	43.0%
SAU802070	BPT100200	30%	88.7%	90.1%
SAU802070	BBU100159	28%	93.7%	96.2%
SAU802070	BCE100962	30%	85.9%	93.2%
SAU802070	BCE103071	30%	91.4%	95.5%
SAU802070	BFU105069	28%	92.4%	96.6%
SAU802070	BMA104109	30%	91.4%	95.5%
SAU802070	CJU100836	28%	87.4%	91.2%
SAU802070	CAC101046	27%	93.2%	90.9%
SAU802070	CAC102016	38%	95.5%	96.1%
SAU802070	CBO102786	36%	95.5%	94.3%
SAU802070	CDF103831	37%	97.6%	97.1%
SAU802070	CDP100053	31%	93.2%	94.5%
SAU802070	EBC104213	32%	95.3%	99.7%
SAU802070	EFA200474	38%	95.5%	98.9%
SAU802070	EFM101678	32%	94.2%	100%
SAU802070	ECO103947	32%	95.3%	99.7%
SAU802070	HIN101543	32%	95.3%	99.2%
SAU802070	HPY100925	33%	94.8%	98.9%
SAU802070	KPN308841	32%	95.3%	99.7%
SAU802070	LPN103528	31%	56.5%	99.1%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802070	LMO100444	40%	95.3%	98.4%
SAU802070	MCA100312	29%	95.3%	97.4%
SAU802070	MAV105645	33%	93.7%	93.4%
SAU802070	MBV101134	32%	94.8%	99.7%
SAU802070	MLP100239	31%	93.7%	94.1%
SAU802070	MTU203377	32%	94.8%	90.4%
SAU802070	NGO101532	33%	93.2%	97.7%
SAU802070	NME201757	33%	93.2%	97.7%
SAU802070	PMU100413	33%	92.7%	96.4%
SAU802070	PRT101882	32%	95.3%	99.2%
SAU802070	PAE204925	33%	94.8%	99.2%
SAU802070	PPU103159	34%	94.8%	98.9%
SAU802070	PSY101164	33%	95.3%	99.4%
SAU802070	SPA101756	31%	94.0%	98.6%
SAU802070	STY102270	31%	95.3%	99.7%
SAU802070	STM102809	31%	95.3%	99.7%
SAU802070	SAU802070	100%	100%	100%
SAU802070	SEP201329	70%	100%	100%
SAU802070	SHA101048	68%	100%	100%
SAU802070	SMU101166	39%	98.2%	99.7%
SAU802070	SPN401539	38%	93.5%	94.9%
SAU802070	SPY201387	37%	96.3%	100%
SAU802070	TPA100673	33%	86.6%	96.4%
SAU802070	VCH100367	33%	96.3%	96.3%
SAU802070	YPS002811	31%	94.8%	98.9%
SAU802071	BAN108531	48%	22.7%	35.1%
SAU802071	BAN107463	51%	99.2%	99.2%
SAU802071	BPT102423	32%	96.6%	83.7%
SAU802071	BBU100010	30%	93.3%	96.8%
SAU802071	BCE113308	32%	98.3%	90.3%
SAU802071	BFU105262	28%	95.8%	80.4%
SAU802071	BMA102365	33%	95.8%	88.8%
SAU802071	CJU101328	33%	92.4%	97.4%
SAU802071	CPN200439	37%	95.0%	95.9%
SAU802071	CTR200370	35%	94.1%	93.6%
SAU802071	CAC100902	37%	96.6%	98.4%
SAU802071	CBO101228	39%	96.6%	97.6%
SAU802071	CDF100783	40%	94.1%	94.4%
SAU802071	CDP101322	31%	92.4%	96.9%
SAU802071	EBC102618	37%	95.8%	97.6%
SAU802071	EFA203222	48%	96.6%	98.3%
SAU802071	ECO102514	38%	95.8%	97.6%
SAU802071	HPY100795	34%	95.0%	97.5%
SAU802071	KPN303138	38%	95.8%	97.6%
SAU802071	LMO100718	46%	96.6%	99.2%
SAU802071	MAV106414	25%	95.8%	96.9%
SAU802071	MBV101363	25%	95.8%	96.9%
SAU802071	MLP100741	28%	95.8%	96.9%
SAU802071	MTU202486	25%	95.8%	96.9%
SAU802071	MGE100215	34%	53.8%	55.3%
SAU802071	MPN100538	36%	54.6%	55.5%
SAU802071	NGO101699	41%	77.3%	72%
SAU802071	NME201879	36%	97.5%	100%
SAU802071	PRT105767	40%	96.6%	98.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802071	SPA103323	39%	95.8%	97.6%
SAU802071	STY102100	39%	95.8%	97.6%
SAU802071	SAU802071	100%	100%	100%
SAU802071	SEP201331	70%	98.3%	99.1%
SAU802071	SHA101047	75%	97.5%	98.3%
SAU802071	SMU101169	34%	98.3%	98.3%
SAU802071	SPN401540	37%	98.3%	97.5%
SAU802071	SPY201388	41%	96.6%	97.5%
SAU802071	TPA100819	32%	96.6%	96.8%
SAU802071	UUR100396	32%	95.0%	92.2%
SAU802071	VCH102421	41%	97.5%	99.2%
SAU802071	YPS003414	34%	95.8%	97.6%
SAU802075	ABA101351	40%	98.4%	91.5%
SAU802075	BPT102678	39%	97.8%	93.5%
SAU802075	EBC100703	36%	99.5%	99.0%
SAU802075	ECO100679	36%	100%	100%
SAU802075	KPN302575	37%	100%	99.5%
SAU802075	PPU106278	36%	97.3%	97.8%
SAU802075	STY101873	39%	97.8%	95.4%
SAU802075	SAU802075	100%	100%	100%
SAU802075	YPS001486	39%	97.8%	93%
SAU802076	ABA101353	55%	99.6%	99.0%
SAU802076	BAN101555	47%	99.3%	100%
SAU802076	BAN105989	60%	99.3%	96.1%
SAU802076	BFR10818	54%	98.8%	98.5%
SAU802076	BPT102676	51%	99.0%	95.3%
SAU802076	BFU106360	57%	45.9%	97.8%
SAU802076	BMA100646	54%	98.4%	94.4%
SAU802076	CJU100628	59%	98.5%	97.7%
SAU802076	CAC103333	61%	98.8%	97.8%
SAU802076	CDF103879	61%	99.0%	97.4%
SAU802076	EBC100702	55%	54.8%	99.2%
SAU802076	EFA201049	54%	97.8%	98.8%
SAU802076	EFM100911	24%	86.5%	76.0%
SAU802076	ECO100680	55%	98.4%	97.9%
SAU802076	KPN302573	54%	97.9%	97.5%
SAU802076	LMO102824	55%	97.3%	97.9%
SAU802076	MAV101812	53%	96.4%	93.4%
SAU802076	MBV104268	53%	98.4%	95.3%
SAU802076	MTU201019	53%	98.4%	95.2%
SAU802076	PRT102410	53%	98.4%	98.4%
SAU802076	PAE201633	54%	97.2%	94.5%
SAU802076	PPU106277	54%	97.2%	98.9%
SAU802076	PSY105755	55%	97.2%	94.2%
SAU802076	SPA100439	44%	95.6%	98.8%
SAU802076	STY101874	58%	16.4%	0.7%
SAU802076	SAU800073	71%	100%	100%
SAU802076	SAU802076	100%	100%	100%
SAU802076	SEP200654	71%	100%	100%
SAU802076	YPS001489	55%	99.3%	98.8%
SAU802081	ABA101163	40%	70.4%	60%
SAU802081	BAN102211	42%	95.3%	99.4%
SAU802081	BAN103847	50%	98.4%	95.5%
SAU802081	BFR10255	37%	88.7%	72.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802081	BPT100457	40%	71.7%	64.3%
SAU802081	BCE107115	39%	76.1%	93.7%
SAU802081	BFU107954	39%	74.3%	81.6%
SAU802081	BMA103404	40%	75.1%	84.7%
SAU802081	CAC103020	44%	83.6%	80.7%
SAU802081	CBO102910	46%	81.8%	84.3%
SAU802081	CDF103369	41%	88.9%	84.0%
SAU802081	CDP101075	39%	92.3%	83.7%
SAU802081	EBC103897	40%	90.3%	73.9%
SAU802081	EFA200476	49%	97.0%	96.5%
SAU802081	EFM201829	50%	95.7%	99.6%
SAU802081	ECO103094	39%	92.5%	73.2%
SAU802081	HIN100222	37%	93.3%	76.0%
SAU802081	HPY100243	35%	92.7%	95.5%
SAU802081	KPN300133	44%	29.1%	99.3%
SAU802081	KPN301427	39%	92.1%	73.9%
SAU802081	LPN103085	38%	97.6%	84.6%
SAU802081	LMO100391	50%	98.4%	98.1%
SAU802081	MCA100979	33%	97.0%	85.5%
SAU802081	MAV100272	39%	87.4%	78.1%
SAU802081	MBV105490	38%	90.7%	79.4%
SAU802081	MLP100490	32%	92.5%	90.3%
SAU802081	MTU201236	38%	90.7%	79.4%
SAU802081	MGE100435	32%	71.3%	82.2%
SAU802081	MPN100219	34%	72.1%	83.1%
SAU802081	NGO101914	38%	71.1%	87.4%
SAU802081	NME201494	38%	71.1%	80.5%
SAU802081	PMU101112	39%	93.3%	76.4%
SAU802081	PRT102432	39%	90.7%	75.1%
SAU802081	PAE202838	39%	90.7%	81.5%
SAU802081	PPU101891	40%	90.1%	79.8%
SAU802081	PSY103180	39%	91.7%	81.9%
SAU802081	SPA101061	40%	79.4%	86.7%
SAU802081	STY100977	39%	92.5%	73.2%
SAU802081	STM102125	37%	72.5%	82.2%
SAU802081	SAU802081	100%	100%	100%
SAU802081	SEP201342	87%	100%	100%
SAU802081	SHA100953	87%	100%	100%
SAU802081	SMU100751	48%	97.2%	95.9%
SAU802081	SPN401439	47%	96.2%	96.6%
SAU802081	SPY201084	46%	98.2%	94.4%
SAU802081	TPA100762	38%	84.0%	65.6%
SAU802081	VCH103524	36%	99.2%	72.2%
SAU802081	YPS001037	39%	92.7%	71.7%
SAU802082	ABA100930	31%	96.0%	93.3%
SAU802082	BAN107253	30%	74.6%	76.8%
SAU802082	BAN102625	49%	36.5%	67.5%
SAU802082	BAN103946	49%	37.2%	98.2%
SAU802082	BAN106298	45%	99.6%	99.8%
SAU802082	BFR103444	40%	44.7%	86.4%
SAU802082	BPT104540	34%	22.1%	40%
SAU802082	BBU100303	28%	94.5%	94.4%
SAU802082	BCE104414	30%	81.6%	97.7%
SAU802082	BFU100824	30%	94.5%	91.9%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802082	BMA104638	31%	99.6%	97.2%
SAU802082	CJU100734	26%	60.2%	55.2%
SAU802082	CPN200950	29%	97.1%	98.2%
SAU802082	CTR200132	28%	96.2%	94.5%
SAU802082	CAC101153	41%	93.8%	93.4%
SAU802082	CBO102608	39%	99.6%	98.7%
SAU802082	CDF103288	38%	94.7%	94.7%
SAU802082	CDP101279	29%	93.8%	93.8%
SAU802082	EBC102572	33%	99.6%	98.7%
SAU802082	EFA200478	42%	94.2%	94.1%
SAU802082	EFM201777	39%	99.3%	99.1%
SAU802082	ECO100086	31%	99.6%	98.7%
SAU802082	HIN101108	33%	94.7%	94.1%
SAU802082	HPY100728	25%	59.3%	52.9%
SAU802082	KPN301858	31%	99.6%	98.7%
SAU802082	LMO101402	41%	95.8%	95.6%
SAU802082	MCA100820	31%	92.7%	91.5%
SAU802082	MAV103997	26%	59.1%	91.1%
SAU802082	MLP100565	26%	99.8%	98.6%
SAU802082	MTU202123	28%	100%	98.2%
SAU802082	NGO100600	35%	94.7%	98.4%
SAU802082	NME201912	34%	94.7%	94.9%
SAU802082	PMU100138	32%	99.6%	98.7%
SAU802082	PRT102642	34%	98.7%	97.2%
SAU802082	PAE204414	32%	93.8%	92.8%
SAU802082	PPU111733	35%	93.6%	92.5%
SAU802082	PSY103854	35%	93.8%	93.6%
SAU802082	SPA102755	32%	99.6%	98.7%
SAU802082	STY103172	32%	99.6%	98.7%
SAU802082	STM102864	32%	99.6%	98.7%
SAU802082	SAU802082	100%	100%	100%
SAU802082	SEP201343	71%	99.8%	100%
SAU802082	SHA100952	73%	99.8%	100%
SAU802082	SMU100741	37%	99.3%	99.6%
SAU802082	SPN401513	33%	95.1%	94.5%
SAU802082	SPY201087	38%	94.5%	92.7%
SAU802082	TPA100382	32%	92.9%	92.6%
SAU802082	VCH102370	33%	99.6%	98.9%
SAU802082	YPS000994	32%	99.6%	98.7%
SAU802083	ABA100626	31%	94.9%	96.1%
SAU802083	BAN104177	35%	86.5%	99.7%
SAU802083	BAN100572	50%	96.9%	99.7%
SAU802083	BFR105381	28%	94.7%	98.8%
SAU802083	BPT102997	31%	93.0%	92.7%
SAU802083	BBU100199	36%	96.3%	98.0%
SAU802083	BCE105651	28%	94.1%	95.2%
SAU802083	BFU100405	31%	94.1%	94.3%
SAU802083	BMA105987	32%	69.9%	81.3%
SAU802083	CJU100737	29%	86.5%	87.0%
SAU802083	CPN200944	32%	97.5%	42.5%
SAU802083	CTR100467	31%	97.8%	42.7%
SAU802083	CAC100277	44%	96.3%	99.1%
SAU802083	CBO101170	28%	94.9%	98.3%
SAU802083	CDF102256	34%	95.5%	99.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802083	CDP100271	37%	94.4%	94.5%
SAU802083	EBC102757	43%	96.9%	96.7%
SAU802083	EFA200480	47%	95.2%	98.9%
SAU802083	EFM201399	47%	96.6%	97.5%
SAU802083	ECO100373	42%	96.9%	97.3%
SAU802083	HIN101114	30%	95.8%	99.0%
SAU802083	HPY100726	27%	97.2%	99.1%
SAU802083	KPN306468	42%	96.9%	97.3%
SAU802083	LPN102747	35%	93.0%	98.0%
SAU802083	LMO102338	48%	99.4%	99.5%
SAU802083	MCA100898	29%	93.5%	86.8%
SAU802083	MAV101441	36%	95.2%	96.5%
SAU802083	MBV102041	36%	94.4%	98.6%
SAU802083	MLP101024	38%	95.2%	93.8%
SAU802083	MTU202943	36%	95.2%	95.4%
SAU802083	NGO100582	29%	94.4%	97.0%
SAU802083	NME201904	29%	94.4%	97.0%
SAU802083	PMU100144	30%	96.3%	98.7%
SAU802083	PRT104171	43%	100%	99.7%
SAU802083	PAE204198	30%	97.8%	98.0%
SAU802083	PPU100215	35%	95.2%	96.9%
SAU802083	PSY105197	47%	77.2%	83.8%
SAU802083	SPA103191	43%	96.9%	97.2%
SAU802083	STY104599	43%	96.9%	97.3%
SAU802083	STM102890	32%	94.9%	99.0%
SAU802083	SAU802083	100%	100%	100%
SAU802083	SEP201344	86%	100%	99.7%
SAU802083	SHA100951	84%	100%	100%
SAU802083	SMU100736	47%	98.6%	99.4%
SAU802083	SPN401514	46%	97.5%	98.6%
SAU802083	SPY201088	45%	98.6%	99.4%
SAU802083	TPA100662	37%	95.5%	88.4%
SAU802083	VCH103296	29%	94.9%	97.6%
SAU802083	YPS001018	35%	94.9%	99.0%
SAU802087	ABA104996	31%	85.6%	87.9%
SAU802087	BAN100950	43%	73.2%	84.5%
SAU802087	BAN106687	42%	91.8%	89%
SAU802087	BCE103740	37%	83.5%	89.0%
SAU802087	BFU100478	34%	90.7%	97.8%
SAU802087	CAC102114	38%	75.3%	76.8%
SAU802087	CBO100308	38%	91.8%	97.8%
SAU802087	CDF100513	40%	99.0%	100%
SAU802087	EBC103158	38%	61.9%	65.9%
SAU802087	ECO102064	31%	90.7%	97.8%
SAU802087	KPN302400	23%	90.7%	77.2%
SAU802087	LMO101992	41%	82.5%	81.4%
SAU802087	MAV104011	47%	97.9%	87.4%
SAU802087	MBV102694	56%	74.2%	75%
SAU802087	MLP101543	51%	81.4%	58.5%
SAU802087	MTU200189	56%	74.2%	75%
SAU802087	PAE201297	35%	84.5%	90.1%
SAU802087	PPU106096	31%	80.4%	83.2%
SAU802087	PSY106346	28%	99.0%	97.9%
SAU802087	SPA103443	30%	90.7%	97.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802087	STY104085	31%	90.7%	97.8%
SAU802087	SAU802087	100%	100%	100%
SAU802087	SEP201349	84%	100%	100%
SAU802087	SHA100794	87%	100%	100%
SAU802090	ABA100996	31%	68.6%	31.4%
SAU802090	BAN110101	33%	42.8%	98.4%
SAU802090	BAN111360	27%	84.1%	92.3%
SAU802090	BAN113573	32%	84.1%	92.5%
SAU802090	BFR11357	28%	69.3%	33.3%
SAU802090	BPT100635	24%	70.7%	33.4%
SAU802090	BBU100441	25%	67.6%	36.9%
SAU802090	BCE114096	27%	70%	34.9%
SAU802090	BFU101036	27%	66.2%	32.1%
SAU802090	BMA108265	29%	66.2%	31.7%
SAU802090	CJU100888	31%	77.2%	39.6%
SAU802090	CPN200442	29%	72.1%	27.3%
SAU802090	CTR200515	30%	71.7%	27.4%
SAU802090	CAC102265	31%	82.1%	87.8%
SAU802090	CBO101415	31%	73.8%	92.6%
SAU802090	CDF102839	31%	70.7%	89.4%
SAU802090	CDP101656	29%	33.8%	27.1%
SAU802090	EBC104228	29%	65.2%	32.0%
SAU802090	EFA200401	37%	86.2%	80%
SAU802090	EFM202652	32%	95.9%	97.7%
SAU802090	ECO103626	29%	70.7%	34.5%
SAU802090	HIN100982	29%	70%	34.4%
SAU802090	HPY101429	29%	71.0%	35.1%
SAU802090	KPN302215	28%	65.2%	32.6%
SAU802090	LMO100776	36%	92.8%	98.5%
SAU802090	MCA103022	33%	71.4%	35.1%
SAU802090	MAV100557	30%	38.6%	28.6%
SAU802090	MBV106261	30%	38.6%	27.6%
SAU802090	MLP101603	29%	38.6%	26.6%
SAU802090	MTU203866	30%	38.6%	27.6%
SAU802090	MGE100473	23%	80.3%	67.8%
SAU802090	MPN100162	22%	69.7%	57.4%
SAU802090	NGO101427	32%	72.4%	36.1%
SAU802090	NME200508	31%	72.4%	36.1%
SAU802090	PMU101165	29%	70%	34.4%
SAU802090	PRT103088	27%	65.2%	32.7%
SAU802090	PAE205563	27%	72.8%	34.3%
SAU802090	PPU103675	26%	73.1%	35.5%
SAU802090	PSY103555	26%	65.2%	31.0%
SAU802090	SPA101311	29%	70.7%	35.4%
SAU802090	STY103946	28%	70.7%	34.5%
SAU802090	STM100542	28%	70.7%	34.5%
SAU802090	SAU802090	100%	100%	100%
SAU802090	SEP201891	83%	100%	100%
SAU802090	SHA100992	74%	59.3%	100%
SAU802090	SMU100510	35%	96.9%	91.9%
SAU802090	SPN401788	29%	100%	95.8%
SAU802090	SPY200255	35%	81.0%	75.2%
SAU802090	TPA100939	25%	70.7%	31.9%
SAU802090	UUR100609	22%	77.2%	64.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802090	VCH100004	29%	70%	34.4%
SAU802090	YPS003474	28%	65.2%	32.1%
SAU802091	ABA103813	30%	84.5%	86.7%
SAU802091	BAN109630	50%	53.1%	86.7%
SAU802091	BAN104683	47%	93.9%	90.4%
SAU802091	BFR11309	29%	83.6%	88.7%
SAU802091	BPT102398	32%	81.7%	81.6%
SAU802091	BCE108732	26%	79.8%	62.7%
SAU802091	BFU102896	27%	68.1%	40.1%
SAU802091	BMA102974	27%	84.0%	48.8%
SAU802091	CJU101007	31%	93.4%	91.0%
SAU802091	CAC102203	29%	83.1%	86.7%
SAU802091	CAC102661	37%	86.4%	85.3%
SAU802091	CBO102722	36%	86.4%	88.3%
SAU802091	CDF102363	39%	34.3%	45.7%
SAU802091	CDF103547	36%	92.5%	91.9%
SAU802091	CDP101293	30%	91.5%	89.2%
SAU802091	EBC103905	26%	80.8%	81.3%
SAU802091	EFA200774	29%	93.0%	91.0%
SAU802091	EFM201656	34%	19.2%	24.0%
SAU802091	ECO103891	28%	79.8%	79.6%
SAU802091	HIN100397	41%	96.7%	95.1%
SAU802091	HPY100830	40%	93.4%	94.5%
SAU802091	KPN302487	28%	79.8%	79.6%
SAU802091	LMO100703	47%	95.3%	95.8%
SAU802091	MCA101998	26%	72.8%	70.5%
SAU802091	MAV101591	30%	81.7%	80.7%
SAU802091	MBV106116	34%	80.3%	80.2%
SAU802091	MLP100208	32%	79.8%	76.6%
SAU802091	MTU200413	34%	80.3%	80.2%
SAU802091	NGO101027	28%	83.1%	85.4%
SAU802091	NME200337	28%	85.0%	87.3%
SAU802091	PMU101260	43%	93.9%	94.1%
SAU802091	PRT101551	29%	81.7%	80%
SAU802091	PAE203973	27%	86.4%	87.6%
SAU802091	PPU107618	29%	85.9%	86.5%
SAU802091	PSY105102	32%	85.9%	87.3%
SAU802091	SPA100267	29%	62.9%	63.8%
SAU802091	STY102650	28%	79.8%	79.6%
SAU802091	SAU802091	100%	100%	100%
SAU802091	SEP201892	61%	99.1%	99.1%
SAU802091	SHA100076	64%	92.5%	100%
SAU802091	SPN400630	52%	98.1%	99.5%
SAU802091	VCH100062	26%	85.9%	43.9%
SAU802091	YPS000460	29%	82.2%	80.5%
SAU802092	ABA100604	38%	94.7%	89.8%
SAU802092	BAN109533	33%	90.9%	89.2%
SAU802092	BAN107336	40%	90.9%	89.2%
SAU802092	CAC103654	34%	93.5%	93.4%
SAU802092	CBO102672	34%	98.5%	97.7%
SAU802092	CDF103521	36%	94.3%	93.9%
SAU802092	EBC100699	40%	95.1%	96.5%
SAU802092	EFA200773	32%	81.4%	80.9%
SAU802092	ECO102063	40%	91.3%	90.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802092	HIN100395	41%	98.5%	97.7%
SAU802092	HPY100832	36%	92.0%	89.0%
SAU802092	KPN308180	42%	91.3%	91.8%
SAU802092	LMO102897	38%	98.1%	95.9%
SAU802092	PMU101262	40%	97.7%	97.0%
SAU802092	SPA101206	30%	90.1%	91.7%
SAU802092	STY104191	41%	93.5%	91.7%
SAU802092	SAU802092	100%	100%	100%
SAU802092	SEP201893	66%	99.6%	100%
SAU802092	SHA100807	73%	55.1%	99.3%
SAU802092	SPN400629	41%	98.9%	97.4%
SAU802094	ABA101933	26%	96.5%	97.3%
SAU802094	BAN101414	26%	95.6%	97.8%
SAU802094	BAN108931	27%	97.4%	96.1%
SAU802094	CJU100408	21%	95.6%	98.2%
SAU802094	EFA200784	26%	96.5%	99.1%
SAU802094	HIN100338	21%	93.4%	98.6%
SAU802094	HPY101269	22%	93.9%	98.6%
SAU802094	KPN303112	22%	93.4%	94.4%
SAU802094	LMO101829	24%	90.0%	89.7%
SAU802094	PMU101264	21%	95.2%	99.5%
SAU802094	SAU802094	100%	100%	100%
SAU802094	SEP201895	62%	100%	100%
SAU802094	SHA100805	62%	99.6%	99.6%
SAU802094	SPN400634	26%	96.9%	92.2%
SAU802098	ABA101324	50%	91.8%	95.8%
SAU802098	BAN112058	68%	61.0%	98.9%
SAU802098	BAN101529	66%	97.9%	99.3%
SAU802098	BFR100706	45%	97.9%	30.8%
SAU802098	BPT101129	47%	96.6%	97.4%
SAU802098	BCE105358	46%	94.5%	91.0%
SAU802098	BFU107782	44%	95.2%	91.0%
SAU802098	BFU105730	46%	94.5%	90.9%
SAU802098	BMA107929	45%	95.2%	91.6%
SAU802098	CJU100245	40%	96.6%	99.3%
SAU802098	CPN200094	47%	97.3%	94.8%
SAU802098	CTR200808	46%	95.2%	92.8%
SAU802098	CAC102008	52%	91.8%	95.0%
SAU802098	CBO103374	61%	97.3%	98.6%
SAU802098	CDF104046	51%	26.7%	97.5%
SAU802098	CDF101479	59%	58.9%	96.6%
SAU802098	CDF100018	61%	82.9%	100%
SAU802098	EBC103090	60%	30.8%	60%
SAU802098	EBC100023	56%	45.2%	65.7%
SAU802098	EBC100020	56%	45.2%	65.7%
SAU802098	EFA203430	53%	91.8%	95.0%
SAU802098	EFM202041	61%	91.8%	96.4%
SAU802098	ECO100180	46%	91.1%	89.4%
SAU802098	HIN101039	45%	94.5%	93.9%
SAU802098	HPY101356	39%	98.6%	94.3%
SAU802098	KPN301913	46%	91.1%	89.4%
SAU802098	LPN101746	44%	89.7%	92.4%
SAU802098	LMO100873	61%	97.3%	98.6%
SAU802098	MCA100038	43%	95.2%	81.1%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802098	NGO100839	53%	84.9%	84.6%
SAU802098	NME200083	53%	84.9%	84.6%
SAU802098	PMU101995	49%	94.5%	91.4%
SAU802098	PRT101246	48%	91.1%	78.5%
SAU802098	PAE203643	46%	94.5%	97.3%
SAU802098	PPU101164	45%	94.5%	97.3%
SAU802098	PSY104344	46%	94.5%	97.3%
SAU802098	SPA100773	46%	91.1%	89.4%
SAU802098	STY103910	46%	91.1%	89.4%
SAU802098	STM103593	46%	91.1%	89.4%
SAU802098	SAU802098	100%	100%	100%
SAU802098	SEP204192	93%	98.6%	99.3%
SAU802098	SHA100083	91%	39.0%	98.3%
SAU802098	SMU100534	53%	95.2%	98.6%
SAU802098	SPN400384	56%	95.2%	98.6%
SAU802098	SPY201345	55%	93.2%	97.1%
SAU802098	VCH102215	46%	91.1%	88.2%
SAU802098	YPS001148	47%	91.1%	74.6%
SAU802099	SAU802099	100%	100%	100%
SAU802100	ABA104194	50%	93.7%	85.4%
SAU802100	BAN100780	56%	95.3%	83.1%
SAU802100	BAN104280	61%	94.8%	83.2%
SAU802100	BPT102115	49%	95.8%	86.3%
SAU802100	BFU102916	50%	95.0%	79.5%
SAU802100	BMA104589	52%	58.2%	93.3%
SAU802100	CJU100797	46%	93.7%	85.2%
SAU802100	CPN200175	39%	88.5%	74.2%
SAU802100	CTR200730	39%	91.4%	79.4%
SAU802100	CAC103585	46%	96.1%	87.6%
SAU802100	CBO100954	51%	93.7%	85.4%
SAU802100	CDF100485	56%	34.7%	100%
SAU802100	CDF102163	58%	54.6%	97.4%
SAU802100	CDP101476	44%	93.5%	84.7%
SAU802100	EFA201611	58%	94.8%	83.8%
SAU802100	EFM201945	58%	94.8%	83.6%
SAU802100	HIN101057	48%	95.0%	85.6%
SAU802100	KPN103684	47%	95.0%	86.4%
SAU802100	LPN103006	49%	93.7%	85.1%
SAU802100	LMO101018	60%	94.8%	83.7%
SAU802100	MCA100762	48%	93.7%	85.2%
SAU802100	MAV106518	45%	51.4%	98.0%
SAU802100	MBV100208	43%	93.5%	84.7%
SAU802100	MLP100716	43%	93.5%	84.7%
SAU802100	MTU201298	43%	93.5%	84.7%
SAU802100	NME200242	49%	95.0%	86.3%
SAU802100	PMU100180	48%	95.0%	85.4%
SAU802100	PPU109849	49%	93.7%	85.3%
SAU802100	SPA100963	47%	41.8%	99.4%
SAU802100	SAU802100	100%	100%	100%
SAU802100	SEP202410	88%	94.8%	86.2%
SAU802100	SHA101060	86%	88.0%	100%
SAU802100	SMU100515	55%	93.7%	85.1%
SAU802100	SPN401779	56%	93.7%	84.3%
SAU802100	SPY200561	56%	93.7%	85.1%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802100	VCH102478	50%	48.8%	93.3%
SAU802105	ABA102336	55%	95.0%	94.9%
SAU802105	BAN102895	65%	100%	100%
SAU802105	BAN104850	79%	100%	100%
SAU802105	BFR12383	55%	95.8%	95.8%
SAU802105	BPT102265	60%	98.8%	99.2%
SAU802105	BCE113271	58%	99.0%	99.4%
SAU802105	BFU111824	59%	99.0%	99.4%
SAU802105	BMA104609	58%	99.0%	99.4%
SAU802105	CJU100094	64%	98.6%	99.2%
SAU802105	CAC101220	64%	100%	99.8%
SAU802105	CBO103759	63%	99.2%	99.2%
SAU802105	CDF103688	67%	99.2%	99.2%
SAU802105	CDP100092	55%	100%	92.6%
SAU802105	EBC104234	53%	99.4%	99.8%
SAU802105	EFA201608	72%	99.4%	96.3%
SAU802105	EFM200643	72%	99.2%	96.1%
SAU802105	ECO103655	54%	96.2%	96.3%
SAU802105	HIN100461	57%	96.8%	96.9%
SAU802105	HPY101117	60%	99.2%	99.4%
SAU802105	KPN301117	54%	96.2%	96.9%
SAU802105	LPN101363	62%	74.1%	99.2%
SAU802105	LMO102357	77%	100%	99.6%
SAU802105	MCA100632	57%	98.2%	98.4%
SAU802105	MAV106522	58%	99.4%	91.9%
SAU802105	MBV105525	57%	99.4%	92.7%
SAU802105	MLP100709	57%	99.4%	91.2%
SAU802105	MTU201291	57%	99.4%	92.7%
SAU802105	MGE100413	55%	91.6%	88.8%
SAU802105	MPN100242	56%	91.6%	88.8%
SAU802105	NGO101344	57%	99.4%	99.4%
SAU802105	NME200481	57%	99.4%	99.4%
SAU802105	PMU101492	55%	96.8%	96.9%
SAU802105	PRT105365	55%	95.4%	95.5%
SAU802105	PAE205551	56%	95.8%	95.7%
SAU802105	PPU103565	56%	95.8%	95.7%
SAU802105	PSY106861	59%	86.9%	95.9%
SAU802105	SPA103402	53%	42.2%	99.5%
SAU802105	STY103858	55%	96.2%	96.3%
SAU802105	SAU802105	100%	100%	100%
SAU802105	SEP201899	94%	100%	99.8%
SAU802105	SHA101055	94%	100%	100%
SAU802105	SMU101004	72%	98.6%	98.8%
SAU802105	SPN401361	72%	98.4%	98.6%
SAU802105	SPY200556	72%	98.8%	98.8%
SAU802105	UUR100131	57%	97.0%	61.0%
SAU802105	VCH102727	57%	96.2%	94.5%
SAU802105	YPS003553	55%	96.2%	96.3%
SAU802106	ABA105713	25%	97.2%	96.6%
SAU802106	BAN113283	31%	97.2%	96.1%
SAU802106	BPT104652	28%	94.4%	93.9%
SAU802106	BCE113381	29%	96.1%	95.5%
SAU802106	BFU106431	28%	96.1%	95.5%
SAU802106	BMA109247	28%	96.1%	95.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802106	CAC100509	20%	93.3%	92.7%
SAU802106	CBO103858	24%	93.3%	92.7%
SAU802106	CDF100340	24%	97.8%	96.7%
SAU802106	CDP100090	19%	91.1%	59.0%
SAU802106	EBC104237	27%	95.0%	94.4%
SAU802106	EFA203407	21%	95.5%	94.4%
SAU802106	EFM202376	21%	97.2%	96.1%
SAU802106	ECO103656	25%	95.0%	94.4%
SAU802106	HIN100462	23%	98.3%	97.7%
SAU802106	KPN301116	28%	95.0%	94.4%
SAU802106	LPN103596	27%	93.9%	93.3%
SAU802106	LMO101750	30%	97.8%	97.2%
SAU802106	MCA100631	24%	96.1%	95.6%
SAU802106	MGE100414	22%	95.5%	97.7%
SAU802106	MPN100241	20%	96.1%	97.2%
SAU802106	NGO103629	28%	93.9%	93.2%
SAU802106	NME200480	27%	93.9%	93.2%
SAU802106	PMU101491	22%	98.3%	97.7%
SAU802106	PRT104944	25%	93.9%	93.2%
SAU802106	PAE205552	23%	95.5%	94.9%
SAU802106	PPU103564	26%	66.5%	79.7%
SAU802106	PSY103436	24%	93.9%	96.5%
SAU802106	SPA103404	26%	95.0%	94.4%
SAU802106	STY107267	27%	95.0%	94.4%
SAU802106	SAU802106	100%	100%	100%
SAU802106	SEP201900	64%	100%	100%
SAU802106	SHA101054	58%	100%	100%
SAU802106	SMU101006	21%	96.6%	96.1%
SAU802106	SPN401362	24%	93.3%	92.7%
SAU802106	SPY200555	22%	90.5%	89.9%
SAU802106	UUR100133	19%	96.6%	96.6%
SAU802106	VCH102728	23%	95.5%	94.9%
SAU802106	YPS003556	24%	95.0%	94.4%
SAU802107	ABA102339	24%	84.4%	93.6%
SAU802107	BAN100824	42%	94.8%	96.4%
SAU802107	BAN112818	42%	94.8%	96.4%
SAU802107	BFR102691	28%	87.3%	92.1%
SAU802107	BPT104649	23%	84.4%	93.6%
SAU802107	BCE107096	24%	83.8%	99.3%
SAU802107	BFU106432	24%	86.7%	96.2%
SAU802107	BMA103063	24%	83.8%	99.3%
SAU802107	CJU100091	20%	74.6%	91.5%
SAU802107	CPN200676	36%	41.6%	35.1%
SAU802107	CAC100986	31%	87.9%	95.6%
SAU802107	CBO100440	29%	87.3%	95.0%
SAU802107	CDF103938	31%	91.3%	91.8%
SAU802107	CDP100088	25%	93.1%	83.5%
SAU802107	EBC105501	28%	86.7%	96.2%
SAU802107	EFA203406	35%	88.4%	86.9%
SAU802107	EFM201470	34%	96.0%	95.4%
SAU802107	ECO103657	26%	86.7%	96.2%
SAU802107	HIN100463	23%	86.7%	96.2%
SAU802107	HPY201061	21%	66.5%	72.2%
SAU802107	KPN306143	28%	42.8%	45.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802107	LPN102324	21%	89.0%	60.7%
SAU802107	LMO102155	35%	94.8%	95.3%
SAU802107	MCA100630	25%	84.4%	94.2%
SAU802107	MAV106520	21%	79.2%	77.0%
SAU802107	MBV105523	21%	86.7%	33.9%
SAU802107	MLP100708	24%	86.7%	33.9%
SAU802107	MTU201290	21%	86.7%	33.9%
SAU802107	MGE100415	25%	85.5%	71.2%
SAU802107	MPN100240	25%	85.5%	71.5%
SAU802107	NGO103626	24%	86.7%	96.2%
SAU802107	NME200479	24%	86.7%	96.2%
SAU802107	PMU101490	23%	86.7%	96.2%
SAU802107	PRT106151	26%	86.7%	96.2%
SAU802107	PAE205553	26%	86.7%	96.2%
SAU802107	PPU112306	26%	86.7%	96.2%
SAU802107	PSY103435	25%	86.7%	96.2%
SAU802107	SPA103406	27%	86.7%	96.2%
SAU802107	STY107265	27%	86.7%	96.2%
SAU802107	SAU802107	100%	100%	100%
SAU802107	SEP201901	82%	100%	100%
SAU802107	SHA101818	86%	49.7%	100%
SAU802107	SMU101008	36%	91.3%	95.8%
SAU802107	SPN401363	31%	89.0%	93.9%
SAU802107	SPY200554	35%	89.0%	93.9%
SAU802107	UUR100134	28%	85.5%	72.2%
SAU802107	YPS003559	26%	86.7%	96.2%
SAU802109	ABA102343	30%	77.3%	71.1%
SAU802109	BAN101337	53%	12.4%	65.2%
SAU802109	BAN109723	66%	12.4%	83.3%
SAU802109	BAN111963	55%	56.6%	94.4%
SAU802109	BAN106879	55%	93.4%	95.4%
SAU802109	BFR102190	27%	87.6%	59.3%
SAU802109	BPT104642	29%	96.3%	89.1%
SAU802109	BCE101199	27%	94.2%	89.0%
SAU802109	BFU111209	26%	97.5%	93.1%
SAU802109	BFU108338	27%	90.1%	83.5%
SAU802109	BMA102656	26%	97.9%	65.9%
SAU802109	CJU101129	25%	90.9%	91.2%
SAU802109	CAC101894	26%	96.7%	95.9%
SAU802109	CBO100509	33%	100%	100%
SAU802109	CDF102803	31%	89.7%	92.7%
SAU802109	CDP100087	32%	92.6%	74.7%
SAU802109	EBC104246	32%	99.2%	88.6%
SAU802109	EFA203403	50%	93.0%	94.6%
SAU802109	EFM200212	49%	93.0%	94.6%
SAU802109	ECO103659	34%	85.5%	80.4%
SAU802109	HIN100465	32%	87.2%	85.5%
SAU802109	HPY100815	26%	87.6%	87.2%
SAU802109	KPN301113	34%	85.5%	80.4%
SAU802109	LPN100590	35%	64.9%	59.6%
SAU802109	LMO102867	58%	100%	100%
SAU802109	MCA100628	30%	83.5%	77.5%
SAU802109	MAV106517	36%	92.1%	88.5%
SAU802109	MBV105517	35%	92.1%	89.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802109	MLP100705	35%	94.2%	91.2%
SAU802109	MTU201287	35%	92.1%	89.6%
SAU802109	MGE100417	22%	94.6%	81.5%
SAU802109	MPN100238	25%	94.6%	81.2%
SAU802109	NGO101341	27%	94.2%	86.1%
SAU802109	NME200477	28%	94.2%	86.1%
SAU802109	PMU101488	31%	89.3%	86.7%
SAU802109	PRT105765	32%	93.0%	84.7%
SAU802109	PAE205555	28%	89.3%	82.0%
SAU802109	PPU103681	28%	86.8%	92.8%
SAU802109	PSY103433	27%	86.4%	79.6%
SAU802109	SPA103408	32%	97.9%	87.5%
SAU802109	STY103856	32%	97.9%	87.5%
SAU802109	SAU802109	100%	100%	100%
SAU802109	SEP201902	87%	100%	100%
SAU802109	SHA100056	83%	100%	100%
SAU802109	SMU101010	40%	91.7%	91.6%
SAU802109	SPN401364	37%	91.7%	92.4%
SAU802109	SPY200553	36%	91.7%	92.4%
SAU802109	UUR100136	24%	100%	87.3%
SAU802109	VCH102731	30%	63.6%	60%
SAU802109	YPS000004	32%	97.9%	86.5%
SAU802111	ABA105452	42%	96.0%	98.7%
SAU802111	BAN106286	54%	19.7%	94.9%
SAU802111	BAN110258	39%	88.8%	92.9%
SAU802111	BAN112148	60%	96.8%	96.3%
SAU802111	BAN107002	60%	96.8%	98.4%
SAU802111	BFR104545	49%	95.5%	98.9%
SAU802111	BFR12295	46%	96.0%	99.5%
SAU802111	CJU101068	24%	77.9%	79.0%
SAU802111	CAC103461	52%	99.2%	97.9%
SAU802111	CAC103778	55%	97.9%	98.4%
SAU802111	CBO100630	53%	99.2%	94.7%
SAU802111	CDF100919	58%	95.5%	96.3%
SAU802111	EFA200201	60%	99.2%	98.2%
SAU802111	EFM201136	23%	97.3%	96.3%
SAU802111	KPN301893	50%	95.7%	98.1%
SAU802111	LMO102015	60%	99.2%	98.4%
SAU802111	NME200190	50%	94.7%	97.8%
SAU802111	PPU108280	48%	90.7%	96.1%
SAU802111	SAU802111	100%	100%	100%
SAU802111	SEP201903	72%	100%	98.4%
SAU802111	SHA100639	66%	99.7%	99.5%
SAU802111	SMU100328	56%	99.2%	97.9%
SAU802111	SPN300337	57%	95.5%	98.4%
SAU802111	VCH100901	50%	95.5%	98.9%
SAU802111	YPS001517	51%	95.7%	98.1%
SAU802112	ABA105256	52%	81.8%	97.7%
SAU802112	BAN112213	72%	100%	100%
SAU802112	BFR103881	33%	95.2%	94.5%
SAU802112	BPT100985	48%	98.1%	84.4%
SAU802112	BCE107019	56%	97.6%	94.4%
SAU802112	BFU100449	54%	64.6%	100%
SAU802112	BMA105302	56%	97.6%	94.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802112	CJU101210	47%	99.5%	99.5%
SAU802112	CTR200822	52%	99.5%	68.6%
SAU802112	CAC100474	70%	100%	100%
SAU802112	CBO100953	70%	100%	100%
SAU802112	CDF104480	66%	100%	100%
SAU802112	CDP100815	43%	99.0%	97.6%
SAU802112	EBC102719	51%	99.0%	99.5%
SAU802112	EFA201665	70%	100%	100%
SAU802112	EFM100705	72%	54.1%	100%
SAU802112	ECO102449	51%	99.0%	95.4%
SAU802112	HIN101200	52%	96.2%	96.6%
SAU802112	KPN309030	51%	99.0%	99.5%
SAU802112	LPN102459	60%	99.5%	97.2%
SAU802112	LMO102461	71%	100%	100%
SAU802112	MCA103555	52%	98.6%	95.8%
SAU802112	MAV100235	44%	97.6%	79.0%
SAU802112	MBV100852	44%	99.0%	99.5%
SAU802112	MTU203266	44%	99.0%	99.5%
SAU802112	MGE100030	46%	96.2%	97.1%
SAU802112	MPN100121	46%	84.7%	98.9%
SAU802112	NGO100075	50%	98.6%	99.0%
SAU802112	NME200908	50%	98.6%	99.0%
SAU802112	PMU100019	53%	96.2%	96.6%
SAU802112	PRT104353	53%	99.0%	99.5%
SAU802112	PAE204643	53%	98.6%	97.2%
SAU802112	PPU104022	53%	96.2%	94.8%
SAU802112	PSY102376	53%	96.2%	94.8%
SAU802112	SPA103099	50%	99.0%	98.6%
SAU802112	STY101654	51%	99.0%	99.5%
SAU802112	SAU802112	100%	100%	100%
SAU802112	SEP201904	94%	100%	100%
SAU802112	SHA100638	94%	100%	100%
SAU802112	SMU100374	70%	100%	100%
SAU802112	SPN400655	71%	100%	96.8%
SAU802112	SPY200285	70%	100%	100%
SAU802112	TPA100444	34%	42.1%	25%
SAU802112	UUR100115	54%	97.6%	98.6%
SAU802112	VCH102191	52%	99.0%	99.5%
SAU802112	YPS002584	52%	99.0%	99.5%
SAU802113	ABA104851	60%	99.0%	98.1%
SAU802113	BAN101706	68%	99.3%	99.3%
SAU802113	BAN109367	70%	99.8%	99.3%
SAU802113	BFR11177	57%	98.5%	99.3%
SAU802113	BPT102825	62%	98.1%	96.9%
SAU802113	BBU100600	55%	98.1%	99.5%
SAU802113	BCE107637	61%	99.8%	98.6%
SAU802113	BFU111760	56%	99.0%	97.4%
SAU802113	BMA102315	60%	99.8%	83.0%
SAU802113	CJU100370	55%	98.3%	97.6%
SAU802113	CPN200229	44%	97.3%	90.5%
SAU802113	CTR200706	44%	97.3%	90.5%
SAU802113	CAC101420	64%	99.3%	98.8%
SAU802113	CBO101302	65%	98.3%	97.3%
SAU802113	CDF100075	65%	17.7%	83.0%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802113	CDF100511	66%	99.3%	97.6%
SAU802113	CDP100921	54%	99.3%	96.0%
SAU802113	EBC100017	57%	27.4%	97.5%
SAU802113	EBC102113	57%	99.0%	97.6%
SAU802113	EFA201664	66%	99.8%	99.8%
SAU802113	EFM103325	62%	11.7%	95.9%
SAU802113	ECO102502	59%	99.0%	98.1%
SAU802113	HIN100869	57%	99.0%	97.9%
SAU802113	HPY100180	53%	99.8%	98.8%
SAU802113	KPN305968	58%	98.1%	97.1%
SAU802113	LPN101884	55%	50.2%	97.7%
SAU802113	LMO102513	70%	99.8%	99.3%
SAU802113	MCA101556	59%	98.3%	96.7%
SAU802113	MAV100777	56%	98.3%	95.8%
SAU802113	MBV106196	54%	99.0%	96.9%
SAU802113	MLP101190	53%	99.0%	96.5%
SAU802113	MTU200070	54%	99.0%	96.9%
SAU802113	MGE100406	54%	96.6%	97.0%
SAU802113	MPN100266	53%	97.6%	98.0%
SAU802113	NGO101181	60%	99.0%	97.8%
SAU802113	NME201154	60%	99.0%	97.8%
SAU802113	PMU100225	57%	99.0%	98.1%
SAU802113	PRT105514	56%	99.0%	98.1%
SAU802113	PAE204600	60%	99.0%	97.8%
SAU802113	PPU107530	60%	98.3%	97.4%
SAU802113	PSY105291	60%	99.0%	97.8%
SAU802113	SPA103023	55%	96.6%	96.2%
SAU802113	STY102040	58%	99.0%	98.1%
SAU802113	SAU802113	100%	100%	100%
SAU802113	SEP201905	87%	99.8%	99.8%
SAU802113	SHA100637	84%	100%	100%
SAU802113	SMU100311	59%	98.3%	96.7%
SAU802113	SPN400928	61%	98.3%	97.1%
SAU802113	SPY200872	60%	98.3%	97.1%
SAU802113	TPA100325	44%	93.4%	72.6%
SAU802113	VCH103010	61%	98.3%	94.0%
SAU802113	YPS003331	57%	99.0%	98.1%
SAU802118	ABA105579	53%	97.8%	96.4%
SAU802118	BAN113068	61%	94.7%	99.1%
SAU802118	BAN100929	65%	98.0%	99.2%
SAU802118	BFR11151	45%	98.3%	97.6%
SAU802118	BPT101750	50%	99.2%	98.3%
SAU802118	BBU100195	47%	98.0%	98.6%
SAU802118	BCE108751	49%	98.9%	98.1%
SAU802118	BFU107325	50%	98.9%	98.1%
SAU802118	BMA103540	50%	99.7%	98.9%
SAU802118	CJU101518	54%	98.0%	98.6%
SAU802118	CPN200648	51%	91.9%	94.7%
SAU802118	CTR200287	52%	92.5%	93.0%
SAU802118	CAC101625	54%	99.2%	99.2%
SAU802118	CBO100481	57%	98.6%	98.9%
SAU802118	CDF101347	58%	97.8%	99.2%
SAU802118	CDP100071	47%	96.6%	97.2%
SAU802118	EBC100920	56%	68.7%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802118	EFA201655	63%	99.4%	100%
SAU802118	EFM200375	61%	99.4%	100%
SAU802118	ECO101184	50%	98.9%	98.1%
SAU802118	HIN101530	51%	98.0%	97.0%
SAU802118	HPY100075	51%	96.4%	97.7%
SAU802118	KPN303478	50%	98.9%	98.1%
SAU802118	LPN101572	54%	96.1%	95.3%
SAU802118	LMO101439	64%	99.2%	99.4%
SAU802118	MCA100127	55%	96.4%	95.8%
SAU802118	MAV106507	42%	97.2%	97.8%
SAU802118	MBV105506	40%	97.2%	97.8%
SAU802118	MLP100700	40%	97.5%	98.1%
SAU802118	MTU201282	40%	97.2%	97.8%
SAU802118	MGE100263	48%	98.3%	97.5%
SAU802118	MPN100475	47%	97.8%	96.9%
SAU802118	NGO100540	53%	99.2%	98.9%
SAU802118	NME201794	53%	99.2%	98.9%
SAU802118	PMU100555	51%	98.9%	98.1%
SAU802118	PRT101055	52%	98.0%	97.2%
SAU802118	PAE204662	52%	99.2%	98.9%
SAU802118	PPU109700	52%	99.2%	98.9%
SAU802118	PSY102423	50%	98.6%	98.3%
SAU802118	SPA100352	44%	98.9%	98.0%
SAU802118	STY101661	50%	98.9%	98.1%
SAU802118	SAU802118	100%	100%	100%
SAU802118	SEP201909	93%	100%	100%
SAU802118	SHA100601	90%	100%	100%
SAU802118	SMU100318	58%	98.9%	99.2%
SAU802118	SPN400924	58%	98.9%	99.2%
SAU802118	SPY200868	57%	99.2%	99.4%
SAU802118	TPA100050	46%	96.6%	98.9%
SAU802118	UUR100003	52%	92.5%	92.2%
SAU802118	VCH102146	52%	98.6%	97.8%
SAU802118	YPS003258	51%	98.0%	97.2%
SAU802119	BAN102071	61%	84.9%	97.7%
SAU802119	BAN101436	63%	95.0%	97.4%
SAU802119	BFR10775	46%	91.5%	87.9%
SAU802119	BBU100790	26%	83.9%	52.3%
SAU802119	CAC102314	60%	95.0%	96.9%
SAU802119	CBO102085	60%	95.0%	99.0%
SAU802119	EBC100656	29%	86.4%	76.3%
SAU802119	EFA201653	28%	92.5%	95.9%
SAU802119	EFM201540	27%	86.9%	90.7%
SAU802119	ECO101209	29%	86.4%	86.3%
SAU802119	HIN100508	29%	86.4%	91.7%
SAU802119	KPN300816	29%	86.4%	86.3%
SAU802119	LPN103251	27%	86.4%	85.2%
SAU802119	LMO102848	29%	88.9%	94.8%
SAU802119	MGE100034	46%	90.5%	83.1%
SAU802119	MPN100110	47%	89.9%	91.1%
SAU802119	PMU101236	29%	86.4%	92.2%
SAU802119	PRT105114	28%	92.5%	95.5%
SAU802119	SPA100526	30%	86.4%	87.2%
SAU802119	STY102989	30%	86.4%	86.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802119	SAU802119	100%	100%	100%
SAU802119	SEP201910	86%	100%	100%
SAU802119	SHA100600	84%	100%	100%
SAU802119	SMU100321	27%	88.9%	91.8%
SAU802119	SPN400922	26%	92.5%	94.0%
SAU802119	SPY200867	29%	86.9%	93.1%
SAU802119	UUR100601	44%	91.5%	83.4%
SAU802119	VCH101148	27%	86.4%	92.2%
SAU802119	YPS000765	27%	86.4%	90.3%
SAU802120	ABA103769	50%	92.9%	91.7%
SAU802120	BAN113559	70%	96.4%	100%
SAU802120	BAN104117	72%	96.4%	100%
SAU802120	BFR11933	43%	94.0%	95.2%
SAU802120	BPT100219	50%	92.9%	61.6%
SAU802120	BBU100228	47%	92.9%	96.3%
SAU802120	BCE110175	49%	98.8%	95.3%
SAU802120	BFU100113	50%	97.6%	92.0%
SAU802120	BMA100597	49%	98.8%	94.3%
SAU802120	CJU100144	35%	96.4%	100%
SAU802120	CPN200649	52%	92.9%	70.6%
SAU802120	CTR200286	47%	92.9%	71.3%
SAU802120	CAC103101	36%	98.8%	98.6%
SAU802120	CBO102930	34%	100%	97.2%
SAU802120	CDF104012	37%	66.7%	79.2%
SAU802120	CDP100131	51%	94.0%	89.8%
SAU802120	EBC103974	49%	94.0%	90.7%
SAU802120	EFA201303	70%	100%	94.4%
SAU802120	ECO100288	46%	94.0%	89.7%
SAU802120	HIN100738	41%	97.6%	97.1%
SAU802120	HPY100544	40%	96.4%	100%
SAU802120	KPN303881	48%	48.8%	71.9%
SAU802120	LMO100203	74%	96.4%	100%
SAU802120	MCA100984	53%	94.0%	90.7%
SAU802120	MAV106531	35%	94.0%	82.5%
SAU802120	MBV105505	34%	94.0%	82.5%
SAU802120	MLP100699	34%	94.0%	78.6%
SAU802120	MTU201281	34%	94.0%	82.5%
SAU802120	MGE100262	28%	92.9%	68.0%
SAU802120	MPN100476	28%	92.9%	68.0%
SAU802120	NGO101307	52%	52.4%	80%
SAU802120	NME201050	45%	92.9%	87.9%
SAU802120	PMU100220	46%	94.0%	90.9%
SAU802120	PRT104831	51%	94.0%	95.1%
SAU802120	PAE203599	51%	92.9%	89.7%
SAU802120	PPU102065	35%	95.2%	93.0%
SAU802120	PSY107166	46%	92.9%	83.9%
SAU802120	SPA100819	45%	94.0%	90.7%
SAU802120	STY104986	46%	94.0%	90.7%
SAU802120	STM100496	46%	94.0%	90.7%
SAU802120	SAU802120	100%	100%	100%
SAU802120	SEP204230	95%	100%	98.8%
SAU802120	SHA102245	81%	65.5%	100%
SAU802120	SMU100284	70%	96.4%	100%
SAU802120	SPN401176	70%	96.4%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802120	SPY200525	67%	100%	96.5%
SAU802120	TPA100252	28%	96.4%	98.5%
SAU802120	VCH100862	50%	94.0%	91.8%
SAU802120	YPS001792	48%	94.0%	90.7%
SAU802121	ABA100304	49%	91.6%	97.1%
SAU802121	BAN105100	51%	94.7%	97.6%
SAU802121	BAN113042	66%	94.7%	97.9%
SAU802121	BFR103103	54%	84.2%	55.7%
SAU802121	BPT100264	51%	91.6%	97.1%
SAU802121	BBU100229	53%	87.4%	74.8%
SAU802121	BCE104048	50%	92.9%	98.1%
SAU802121	BFU105309	51%	90.0%	94.4%
SAU802121	BMA101995	50%	92.9%	98.1%
SAU802121	CJU101081	51%	94.1%	97.7%
SAU802121	CPN200135	53%	91.8%	87.3%
SAU802121	CTR200767	53%	91.3%	96.2%
SAU802121	CAC102868	58%	82.6%	75.4%
SAU802121	CBO103912	55%	96.1%	87.1%
SAU802121	CDF100058	61%	76.7%	67.6%
SAU802121	CDP100068	53%	82.9%	54.4%
SAU802121	EBC103271	59%	60.3%	100%
SAU802121	EFA201306	65%	92.0%	93.7%
SAU802121	ECO103697	52%	93.2%	98.6%
SAU802121	HIN100281	53%	93.2%	98.6%
SAU802121	HPY100543	51%	95.9%	96.6%
SAU802121	KPN301899	53%	86.1%	95%
SAU802121	LMO101598	66%	92.9%	96.7%
SAU802121	MCA100009	40%	42.5%	96.4%
SAU802121	MAV106530	54%	82.6%	61.6%
SAU802121	MBV105502	52%	86.5%	64.0%
SAU802121	MLP100698	51%	86.5%	63.1%
SAU802121	MTU201280	52%	86.5%	64.0%
SAU802121	NGO100759	52%	91.3%	96.7%
SAU802121	NME200762	52%	91.3%	96.7%
SAU802121	PMU101920	52%	93.2%	98.6%
SAU802121	PRT102841	52%	93.2%	98.6%
SAU802121	PAE205234	53%	91.6%	96.9%
SAU802121	PPU100260	52%	90.4%	99.5%
SAU802121	PSY100590	52%	91.6%	96.9%
SAU802121	SPA103748	52%	93.2%	98.6%
SAU802121	STY102102	52%	93.2%	98.6%
SAU802121	STM101036	52%	93.2%	98.6%
SAU802121	SAU802121	100%	100%	100%
SAU802121	SEP201911	95%	100%	100%
SAU802121	SHA100146	94%	99.1%	96.0%
SAU802121	TPA100251	53%	89.0%	75.5%
SAU802121	VCH100303	52%	92.9%	98.3%
SAU802121	YPS001531	51%	93.2%	98.6%
SAU802124	BAN108367	44%	84.2%	83.4%
SAU802124	BAN107764	59%	98.8%	96.7%
SAU802124	BFR11634	34%	97.1%	98.2%
SAU802124	BBU100471	34%	97.1%	94.1%
SAU802124	BCE107676	42%	91.9%	98.2%
SAU802124	CAC102006	50%	98.3%	98.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802124	CBO103182	53%	97.6%	97.6%
SAU802124	EBC101214	42%	97.4%	97.6%
SAU802124	EFA201309	54%	97.6%	95.6%
SAU802124	ECO103119	42%	97.4%	97.6%
SAU802124	HPY100640	40%	98.1%	98.3%
SAU802124	KPN301069	42%	97.4%	97.6%
SAU802124	LMO102733	57%	97.1%	96.2%
SAU802124	MAV102894	37%	52.7%	98.2%
SAU802124	NGO102024	43%	97.6%	98.1%
SAU802124	PRT100966	42%	97.4%	97.4%
SAU802124	PAE204448	44%	97.1%	97.6%
SAU802124	PSY104793	43%	90.7%	98.7%
SAU802124	SPA100481	39%	43.9%	96.9%
SAU802124	STY101491	43%	97.4%	97.6%
SAU802124	SAU802124	100%	100%	100%
SAU802124	SEP201914	85%	100%	100%
SAU802124	SHA101919	83%	100%	100%
SAU802124	SMU101064	51%	97.6%	98.1%
SAU802124	SPN400989	52%	97.6%	98.1%
SAU802124	SPY201041	52%	97.6%	98.1%
SAU802124	TPA100028	31%	98.1%	98.8%
SAU802124	YPS002303	43%	97.4%	97.6%
SAU802125	ABA100914	33%	99.7%	95.4%
SAU802125	BAN112047	72%	97.2%	100%
SAU802125	BAN107884	76%	99.7%	100%
SAU802125	BFR11934	38%	98.6%	96.7%
SAU802125	BPT102002	38%	99.7%	92.9%
SAU802125	BBU100444	26%	94.8%	93.0%
SAU802125	BCE111090	35%	97.9%	92.8%
SAU802125	BFU111409	34%	99.7%	92.7%
SAU802125	BMA102172	35%	97.9%	92.8%
SAU802125	CJU100558	26%	95.1%	93.2%
SAU802125	CAC101944	53%	99.0%	99.7%
SAU802125	CBO101028	43%	96.9%	96.8%
SAU802125	CDF100408	44%	99.3%	99.6%
SAU802125	CDF101639	43%	99.7%	97.9%
SAU802125	CDP101376	30%	92.7%	92.4%
SAU802125	EBC104459	41%	99.7%	100%
SAU802125	EFA201312	48%	99.7%	100%
SAU802125	EFM201171	39%	96.2%	94.8%
SAU802125	ECO102055	42%	99.7%	99.3%
SAU802125	HIN100503	26%	93.0%	91.4%
SAU802125	HPY100173	43%	98.6%	99.3%
SAU802125	KPN306125	51%	98.6%	99.3%
SAU802125	LMO100774	65%	99.7%	100%
SAU802125	MCA100353	34%	99.7%	95.4%
SAU802125	MBV102190	27%	92.7%	92.4%
SAU802125	MLP100198	29%	92.7%	92.2%
SAU802125	MTU200362	27%	92.7%	92.4%
SAU802125	MGE100023	44%	99.0%	99.7%
SAU802125	MPN100129	45%	99.0%	99.7%
SAU802125	NGO101574	35%	99.7%	92.9%
SAU802125	NME200544	35%	99.7%	92.9%
SAU802125	PMU101373	37%	99.7%	98.0%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802125	PRT102752	40%	96.9%	97.2%
SAU802125	PAE200554	34%	99.7%	92.9%
SAU802125	PPU104672	34%	99.7%	94.3%
SAU802125	PSY100210	34%	99.7%	92.9%
SAU802125	SPA103912	43%	97.9%	98.2%
SAU802125	STY100942	43%	97.9%	98.2%
SAU802125	STM101386	43%	97.9%	98.2%
SAU802125	SAU802125	100%	100%	100%
SAU802125	SEP201915	95%	100%	100%
SAU802125	SHA101918	93%	100%	100%
SAU802125	SMU101408	45%	99.7%	100%
SAU802125	SPN400530	44%	99.7%	100%
SAU802125	SPY201455	45%	99.7%	100%
SAU802125	TPA100654	39%	99.0%	97.6%
SAU802125	UUR100603	43%	99.7%	99.3%
SAU802125	VCH100473	26%	89.5%	88.5%
SAU802125	YPS000084	41%	99.3%	99.6%
SAU802130	BAN113149	31%	46.8%	97.0%
SAU802130	BAN107309	36%	97.8%	95.7%
SAU802130	EFA202449	23%	54.7%	10.6%
SAU802130	PSY101953	20%	63.7%	37.3%
SAU802130	SAU802130	100%	100%	100%
SAU802130	SEP201922	75%	99.3%	97.4%
SAU802130	SHA102983	77%	99.3%	99.6%
SAU802133	BAN111842	44%	37.3%	96.7%
SAU802133	BAN109593	58%	49.7%	92.9%
SAU802133	BAN105036	53%	99.2%	97.8%
SAU802133	CAC101783	22%	97.7%	99.5%
SAU802133	CBO102190	27%	97.0%	96.9%
SAU802133	CDF101111	30%	96.7%	93.6%
SAU802133	CDF101575	35%	93.1%	94.2%
SAU802133	CDF100587	38%	97.0%	98.2%
SAU802133	EBC100570	34%	66.5%	63.3%
SAU802133	EFM202575	45%	98.7%	96.6%
SAU802133	ECO101308	33%	66.0%	57.4%
SAU802133	KPN304546	31%	67.0%	58.2%
SAU802133	MAV100227	33%	99.0%	97.2%
SAU802133	MBV100846	33%	95.4%	95.2%
SAU802133	MTU203263	33%	95.4%	95.2%
SAU802133	SAU802133	100%	100%	100%
SAU802133	SEP201928	85%	100%	100%
SAU802133	SHA101910	86%	100%	100%
SAU802137	BAN109977	64%	91.8%	100%
SAU802137	BAN102250	66%	95.9%	95.1%
SAU802137	BFR12234	34%	70.9%	55.4%
SAU802137	BCE105592	55%	57.7%	98.4%
SAU802137	BFU103022	31%	68.6%	47.6%
SAU802137	BFU108762	30%	72.3%	50%
SAU802137	BMA104956	36%	92.3%	81.2%
SAU802137	CAC100384	63%	95.9%	98.6%
SAU802137	CBO100256	58%	96.4%	100%
SAU802137	CDF100310	48%	98.2%	97.7%
SAU802137	CDP101627	45%	95.9%	95.9%
SAU802137	EBC103572	32%	92.7%	84.1%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802137	EFA202355	63%	96.8%	97.3%
SAU802137	EFM201549	62%	96.8%	97.3%
SAU802137	ECO104267	34%	92.7%	83.8%
SAU802137	HIN101089	55%	96.4%	94.6%
SAU802137	KPN308783	35%	92.7%	83.1%
SAU802137	LPN101764	30%	81.8%	72.8%
SAU802137	LMO101987	64%	96.8%	96.0%
SAU802137	MAV103921	45%	48.6%	96.6%
SAU802137	MBV102346	45%	95.9%	95.1%
SAU802137	MLP101461	42%	95.9%	95.1%
SAU802137	MTU200476	45%	95.9%	95.1%
SAU802137	MGE100050	45%	95.9%	94.2%
SAU802137	MPN100091	46%	95.5%	93.3%
SAU802137	PMU101343	55%	96.4%	94.6%
SAU802137	PRT101388	53%	98.6%	98.2%
SAU802137	PAE201382	27%	51.4%	20.5%
SAU802137	PSY100190	32%	76.8%	68.3%
SAU802137	SPA100057	34%	70.5%	83.5%
SAU802137	STY104584	32%	93.2%	82.3%
SAU802137	STM100357	33%	92.7%	81.9%
SAU802137	SAU800138	97%	100%	100%
SAU802137	SAU802137	100%	100%	100%
SAU802137	SEP201938	78%	100%	100%
SAU802137	SHA101905	84%	100%	100%
SAU802137	SMU100919	60%	100%	100%
SAU802137	SPN400745	59%	100%	100%
SAU802137	SPY201436	45%	97.7%	96.0%
SAU802137	TPA100261	41%	93.6%	95.4%
SAU802137	UUR100592	46%	93.2%	95.3%
SAU802137	VCH102315	34%	86.4%	78.0%
SAU802137	YPS001140	53%	97.7%	96.4%
SAU802139	BAN113297	49%	96.6%	98.6%
SAU802139	BAN110089	51%	97.3%	97.9%
SAU802139	BFR12031	33%	82.3%	87.7%
SAU802139	BPT102735	32%	95.2%	75.3%
SAU802139	BBU100689	25%	93.2%	73.5%
SAU802139	BCE107273	33%	98.6%	89.5%
SAU802139	BFU102626	31%	98.6%	67.1%
SAU802139	BMA103777	32%	98.6%	89.5%
SAU802139	CJU101443	27%	95.2%	94.6%
SAU802139	CDP100814	28%	98.6%	90.1%
SAU802139	EBC100875	22%	97.3%	84.4%
SAU802139	EFA200810	28%	92.5%	89.0%
SAU802139	EFA200155	34%	91.8%	88.4%
SAU802139	EFM200208	33%	48.3%	72.4%
SAU802139	ECO100788	23%	97.3%	84.4%
SAU802139	HIN101315	32%	94.6%	86.9%
SAU802139	HPY100239	32%	96.6%	97.2%
SAU802139	KPN300031	20%	78.9%	87.0%
SAU802139	KPN303559	20%	97.3%	84.4%
SAU802139	LMO102910	43%	98.0%	93.6%
SAU802139	MAV101663	24%	92.5%	74.7%
SAU802139	PMU100817	34%	95.9%	88.7%
SAU802139	PRT106088	23%	92.5%	74.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802139	PAE200961	31%	95.9%	90.4%
SAU802139	PPU108680	30%	98.0%	91.7%
SAU802139	PSY105983	33%	98.0%	91.7%
SAU802139	SPA101972	23%	97.3%	84.4%
SAU802139	STY102376	23%	97.3%	84.4%
SAU802139	SAU802139	100%	100%	100%
SAU802139	SEP201942	84%	99.3%	98.6%
SAU802139	SHA101903	84%	98.0%	98.6%
SAU802139	SMU100064	33%	92.5%	78.9%
SAU802139	SPN401429	35%	92.5%	77.0%
SAU802139	SPY201180	33%	91.2%	77.7%
SAU802139	TPA101028	29%	95.2%	79.7%
SAU802139	VCH100138	29%	98.6%	92.9%
SAU802139	YPS000339	23%	93.2%	80.8%
SAU802152	BFR101055	28%	97.9%	98.5%
SAU802152	HPY100644	26%	43.5%	59.4%
SAU802152	SAU802152	100%	100%	100%
SAU802152	SEP201959	69%	99.3%	99.3%
SAU802152	SHA102869	66%	74.0%	99.5%
SAU802152	SPN401123	26%	100%	99.6%
SAU802154	ABA103622	43%	100%	100%
SAU802154	BAN106917	49%	100%	100%
SAU802154	BAN102903	70%	100%	100%
SAU802154	BFR105590	56%	8.2%	33.6%
SAU802154	BPT101720	40%	100%	100%
SAU802154	BCE109254	39%	100%	100%
SAU802154	BFU109440	44%	17.5%	77.9%
SAU802154	BFU103182	40%	100%	100%
SAU802154	BMA102722	39%	100%	100%
SAU802154	CJU101290	36%	100%	100%
SAU802154	CPN200876	38%	100%	100%
SAU802154	CTR200198	38%	100%	100%
SAU802154	CAC103586	45%	100%	100%
SAU802154	CBO102655	43%	100%	100%
SAU802154	CDF100284	44%	100%	100%
SAU802154	CDP100523	40%	96.2%	100%
SAU802154	EBC104245	41%	100%	100%
SAU802154	EFA201749	58%	100%	100%
SAU802154	EFM200906	23%	55.6%	94.0%
SAU802154	ECO103650	41%	100%	100%
SAU802154	HIN100409	39%	100%	100%
SAU802154	HPY101510	37%	100%	100%
SAU802154	KPN300721	40%	100%	100%
SAU802154	LPN102850	38%	100%	100%
SAU802154	LMO101794	65%	100%	100%
SAU802154	MCA103570	37%	100%	100%
SAU802154	MAV105640	40%	100%	96.1%
SAU802154	MBV101159	39%	97.2%	100%
SAU802154	MLP100237	39%	100%	100%
SAU802154	MTU203389	39%	100%	100%
SAU802154	NGO101887	38%	100%	100%
SAU802154	NME200260	38%	100%	100%
SAU802154	PMU101731	39%	100%	100%
SAU802154	PRT104794	42%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802154	PAE205544	42%	100%	100%
SAU802154	PPU102151	43%	100%	100%
SAU802154	PSY103460	42%	100%	100%
SAU802154	SPA101582	38%	100%	100%
SAU802154	STY103864	41%	100%	100%
SAU802154	STM100312	19%	55.9%	94.3%
SAU802154	SAU802154	100%	100%	100%
SAU802154	SEP201962	89%	100%	100%
SAU802154	SHA100979	88%	100%	100%
SAU802154	SMU101007	56%	100%	100%
SAU802154	SPN400245	57%	100%	100%
SAU802154	SPY200983	57%	100%	100%
SAU802154	TPA100852	37%	100%	100%
SAU802154	VCH100482	39%	100%	100%
SAU802154	YPS003544	41%	100%	100%
SAU802158	CAC102954	48%	97.9%	97.3%
SAU802158	CDF104113	44%	100%	99.3%
SAU802158	EBC101475	39%	91.0%	35.1%
SAU802158	EFA201285	44%	93.8%	95.9%
SAU802158	EFM202400	44%	90.3%	92.4%
SAU802158	ECO102128	42%	81.9%	31.6%
SAU802158	HIN100428	40%	89.6%	26.1%
SAU802158	KPN102504	38%	88.9%	67.9%
SAU802158	MPN100189	28%	89.6%	90.2%
SAU802158	PAE100175	41%	84.7%	33.2%
SAU802158	SAU802158	100%	100%	100%
SAU802158	SMU101001	38%	96.5%	98.6%
SAU802158	SPN400358	40%	93.1%	95.2%
SAU802158	YPS001090	36%	92.4%	35.5%
SAU802159	ABA105269	26%	40.5%	44.3%
SAU802159	BCE113957	28%	38.0%	40.6%
SAU802159	BFU102350	25%	56.8%	49.4%
SAU802159	BMA101585	27%	59.5%	47.8%
SAU802159	CAC102601	36%	96.5%	95.3%
SAU802159	CDF104333	39%	98.6%	97.9%
SAU802159	EBC103811	37%	99.5%	98.7%
SAU802159	EFA201284	42%	96.2%	94.8%
SAU802159	EFM200126	42%	96.2%	95.0%
SAU802159	ECO103522	37%	99.7%	99.7%
SAU802159	KPN305795	38%	99.2%	98.4%
SAU802159	MAV108334	28%	58.7%	49.9%
SAU802159	MPN100190	24%	92.1%	90.7%
SAU802159	PMU101062	38%	99.7%	99.2%
SAU802159	PAE202340	24%	45.7%	38.5%
SAU802159	PSY101120	27%	47.6%	39.8%
SAU802159	SPA103111	37%	99.5%	99.5%
SAU802159	STY100406	38%	99.5%	99.5%
SAU802159	STM104137	38%	99.5%	99.5%
SAU802159	SAU802159	100%	100%	100%
SAU802159	SMU100999	41%	99.5%	99.2%
SAU802159	SPN400359	39%	97.8%	98.7%
SAU802159	VCH103762	41%	98.1%	96.1%
SAU802159	YPS003325	37%	99.7%	98.4%
SAU802160	BFR11305	19%	46.2%	73.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802160	BFU115165	25%	6.6%	67.1%
SAU802160	BFU101113	21%	70.6%	97.6%
SAU802160	BMA106913	27%	1.5%	75.4%
SAU802160	EFA200160	23%	20.0%	68.3%
SAU802160	KPN107267	19%	31.6%	61.3%
SAU802160	LMO102026	20%	13.1%	47.4%
SAU802160	MAV105337	19%	21.6%	59.6%
SAU802160	MBV105545	20%	6.9%	59.3%
SAU802160	MLP100688	20%	28.7%	82.7%
SAU802160	MTU201261	20%	6.9%	59.3%
SAU802160	MGE100398	17%	20.0%	48.3%
SAU802160	NME200837	20%	64.2%	38.7%
SAU802160	PPU102763	36%	4.8%	9.4%
SAU802160	PSY104388	20%	7.7%	76.4%
SAU802160	SAU802160	100%	100%	100%
SAU802160	SHA100633	25%	86.9%	70.1%
SAU802160	SHA100651	34%	50.7%	55.8%
SAU802160	SHA101424	30%	35.6%	99.9%
SAU802160	SHA101983	30%	88.4%	10.3%
SAU802160	SPN400581	18%	36.0%	23.2%
SAU802160	SPN401042	20%	6.4%	26.2%
SAU802160	SPY200538	21%	77.2%	47.8%
SAU802161	ABA104792	42%	98.2%	98.7%
SAU802161	BAN112515	62%	76.9%	76.2%
SAU802161	BAN107998	67%	99.8%	100%
SAU802161	BFR11957	24%	96.9%	97.6%
SAU802161	BPT101024	41%	97.3%	98.2%
SAU802161	BCE111154	40%	94.7%	97.9%
SAU802161	BFU108542	38%	64.1%	87.1%
SAU802161	BMA109028	41%	98.0%	98.5%
SAU802161	CJU100328	37%	98.0%	98.0%
SAU802161	CPN200877	43%	98.9%	97.6%
SAU802161	CTR200197	44%	98.4%	96.9%
SAU802161	CAC102696	49%	98.9%	99.6%
SAU802161	CBO100852	48%	99.1%	98.9%
SAU802161	CDF100285	51%	98.7%	95.1%
SAU802161	CDP100049	49%	98.2%	98.7%
SAU802161	EBC102674	45%	98.0%	98.7%
SAU802161	EFA201741	61%	99.8%	100%
SAU802161	EFM202621	25%	93.1%	92.2%
SAU802161	ECO103106	44%	98.0%	98.7%
SAU802161	HIN101431	47%	98.0%	98.4%
SAU802161	HIN101303	47%	98.0%	98.4%
SAU802161	HPY100073	38%	97.3%	98.2%
SAU802161	KPN300882	45%	69.4%	98.4%
SAU802161	LPN103638	45%	97.3%	95.6%
SAU802161	LMO100393	66%	99.8%	99.8%
SAU802161	MCA101170	40%	98.4%	99.1%
SAU802161	MAV103417	48%	98.2%	99.1%
SAU802161	MBV101154	47%	98.2%	99.1%
SAU802161	MLP100234	48%	98.2%	95.2%
SAU802161	MTU203394	47%	98.2%	99.1%
SAU802161	NGO100553	43%	97.8%	98.4%
SAU802161	NME201798	43%	97.8%	98.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802161	PMU100440	47%	98.0%	98.6%
SAU802161	PRT100621	47%	98.0%	98.4%
SAU802161	PAE204745	45%	98.2%	98.7%
SAU802161	PPU108507	45%	97.8%	98.2%
SAU802161	PSY104836	44%	98.2%	98.4%
SAU802161	SPA100515	46%	58.1%	98.5%
SAU802161	STY101478	44%	98.0%	98.7%
SAU802161	SAU802161	100%	100%	100%
SAU802161	SEP201964	92%	100%	100%
SAU802161	SHA100977	88%	99.8%	100%
SAU802161	SMU100302	59%	99.6%	100%
SAU802161	SPN401416	60%	99.8%	100%
SAU802161	SPY200785	60%	99.8%	99.8%
SAU802161	TPA100409	39%	19.3%	13.4%
SAU802161	VCH100627	43%	98.2%	98.4%
SAU802161	YPS001055	45%	98.0%	98.4%
SAU802162	BAN107590	24%	98.1%	66.4%
SAU802162	BAN101871	27%	100%	62.1%
SAU802162	CAC101443	24%	97.7%	74.2%
SAU802162	CBO101794	26%	78.7%	57.7%
SAU802162	CDF103998	23%	97.4%	74.3%
SAU802162	EFA201739	26%	92.6%	74.7%
SAU802162	EFM101102	22%	91.6%	73.5%
SAU802162	LMO100488	34%	41.9%	96.9%
SAU802162	MBV101680	34%	13.9%	12.6%
SAU802162	MTU200828	34%	13.9%	12.6%
SAU802162	NME104849	21%	74.8%	44.1%
SAU802162	SAU802162	100%	100%	100%
SAU802162	SEP201966	70%	100%	99.7%
SAU802162	SHA100469	69%	71.6%	100%
SAU802162	SMU100303	27%	91.0%	89.9%
SAU802162	SPN401417	22%	68.4%	83.4%
SAU802162	SPY200784	23%	93.2%	92.5%
SAU802170	ABA101286	32%	88.6%	93.9%
SAU802170	BAN111561	26%	30.3%	94.5%
SAU802170	BAN110295	30%	88.6%	92.2%
SAU802170	BFR103995	34%	88.2%	95.4%
SAU802170	BBU100117	26%	99.6%	98.7%
SAU802170	BCE107682	31%	86.8%	96.1%
SAU802170	BFU103494	28%	86.8%	96.1%
SAU802170	BMA100077	24%	40.8%	93.1%
SAU802170	CAC102285	35%	89.0%	95.7%
SAU802170	CBO101117	37%	89.0%	94.4%
SAU802170	CDF103680	31%	89.0%	96.3%
SAU802170	CDP100520	24%	83.3%	84.8%
SAU802170	EBC102963	34%	89.9%	93.6%
SAU802170	EFA201192	35%	87.7%	93.1%
SAU802170	EFM100507	33%	87.7%	93.1%
SAU802170	ECO102835	32%	89.9%	93.6%
SAU802170	KPN303348	32%	89.9%	93.6%
SAU802170	LMO101419	31%	92.1%	99.5%
SAU802170	MAV100786	31%	81.1%	56.2%
SAU802170	MBV104176	27%	86.0%	91.7%
SAU802170	MTU201073	27%	86.0%	91.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802170	NGO101498	32%	74.6%	83.2%
SAU802170	NME201751	32%	74.6%	83.2%
SAU802170	PRT102034	30%	36.8%	25.6%
SAU802170	PAE204828	32%	87.3%	96.1%
SAU802170	PPU109350	32%	89.5%	98.5%
SAU802170	PSY103607	34%	71.9%	99.4%
SAU802170	SPA102067	35%	89.0%	94.9%
SAU802170	STY104155	34%	89.9%	93.6%
SAU802170	SAU802170	100%	100%	100%
SAU802170	SEP201988	82%	99.6%	100%
SAU802170	SHA100595	85%	99.6%	100%
SAU802170	SMU100942	54%	93.9%	97.7%
SAU802170	SPN401319	55%	90.4%	95.3%
SAU802170	SPY200885	54%	93.9%	98.6%
SAU802170	TPA101027	38%	88.2%	85.3%
SAU802170	VCH100040	35%	89.5%	94.9%
SAU802170	YPS000173	33%	89.5%	87.6%
SAU802171	CPN200994	30%	97.5%	84.8%
SAU802171	CTR200088	30%	99.0%	86.4%
SAU802171	CAC100688	25%	22.8%	34.9%
SAU802171	EFM202390	26%	22.3%	47.6%
SAU802171	SAU802171	100%	100%	100%
SAU802171	SEP201990	77%	100%	100%
SAU802171	SHA100594	69%	100%	100%
SAU802176	BFR10841	33%	30.9%	98.2%
SAU802176	BFR12085	27%	56.6%	88.4%
SAU802176	BFR102986	27%	93.9%	97.9%
SAU802176	BFR100727	28%	91.8%	96.4%
SAU802176	ECO203932	33%	94.2%	99.4%
SAU802176	KPN103323	29%	88.9%	96.3%
SAU802176	PRT101434	33%	91.3%	96.7%
SAU802176	PSY102146	33%	82.2%	86.6%
SAU802176	SAU802176	100%	100%	100%
SAU802176	SEP202002	72%	100%	100%
SAU802176	SHA100066	71%	100%	100%
SAU802176	SPN400935	35%	94.5%	96.8%
SAU802176	YPS002673	34%	90.7%	94.9%
SAU802177	BAN107236	33%	74.0%	92.0%
SAU802177	BAN102502	33%	88.7%	90.4%
SAU802177	BCE100353	25%	78.3%	75.7%
SAU802177	BFU107408	25%	86.9%	79.7%
SAU802177	BMA101385	44%	29.1%	23.9%
SAU802177	EBC103345	37%	86.2%	89.3%
SAU802177	ECO104179	36%	86.2%	88.7%
SAU802177	KPN304212	25%	76.5%	81.1%
SAU802177	PMU100131	36%	88.4%	92.6%
SAU802177	PSY102144	36%	87.2%	91.6%
SAU802177	SPA100028	29%	33.6%	99.1%
SAU802177	STY103490	26%	73.7%	78.4%
SAU802177	STM103176	26%	73.7%	78.4%
SAU802177	SAU802177	100%	100%	100%
SAU802177	SEP202004	72%	100%	98.8%
SAU802177	SHA100119	69%	52.3%	100%
SAU802177	SPN200521	31%	51.4%	88.1%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802177	VCH100200	25%	86.2%	85.6%
SAU802181	PRT104884	25%	60.6%	62.1%
SAU802181	STM104876	23%	10.2%	38.1%
SAU802181	SAU802181	100%	100%	100%
SAU802181	SEP202012	59%	100%	99.8%
SAU802181	SHA102033	56%	97.7%	98.2%
SAU802183	CBO101399	36%	67.1%	57.6%
SAU802183	EFA203038	29%	77.2%	96.8%
SAU802183	EFM200451	42%	58.2%	75.8%
SAU802183	SAU802183	100%	100%	100%
SAU802183	SEP202016	83%	100%	100%
SAU802183	SHA102688	77%	100%	100%
SAU802183	SPN401622	30%	58.2%	82.1%
SAU802183	SPY200972	36%	77.2%	98.4%
SAU802184	ABA104072	23%	64.6%	95.9%
SAU802184	EFA202511	27%	70.2%	70.4%
SAU802184	MBV100432	45%	17.4%	20.8%
SAU802184	MTU202703	45%	17.4%	20.8%
SAU802184	SAU802184	100%	100%	100%
SAU802184	SEP202018	86%	100%	100%
SAU802184	SHA102031	85%	100%	100%
SAU802186	ABA104325	41%	99.7%	99.4%
SAU802186	BAN104489	40%	23.9%	96.4%
SAU802186	BAN104922	50%	55.2%	98.9%
SAU802186	BAN107319	41%	99.4%	99.7%
SAU802186	BPT100756	31%	59.7%	60.2%
SAU802186	BCE108257	44%	99.7%	94.1%
SAU802186	BFU114209	43%	99.4%	98.5%
SAU802186	BMA103723	26%	91.3%	73.9%
SAU802186	CDP101649	25%	94.3%	95.9%
SAU802186	EBC103573	39%	91.9%	92.5%
SAU802186	EFA202428	31%	83.9%	83.5%
SAU802186	EFM202451	41%	99.7%	96.8%
SAU802186	ECO103945	33%	54.6%	54.4%
SAU802186	KPN306077	40%	91.9%	91.3%
SAU802186	LPN102544	36%	99.7%	98.5%
SAU802186	LMO100089	44%	99.4%	98.8%
SAU802186	MAV101562	32%	55.8%	55.2%
SAU802186	MBV100928	35%	54.3%	54.3%
SAU802186	MLP100086	26%	53.7%	52.1%
SAU802186	MTU201433	35%	54.3%	54.3%
SAU802186	PRT101880	34%	53.7%	53.5%
SAU802186	PAE203565	37%	99.4%	99.1%
SAU802186	PPU100559	38%	99.4%	98.5%
SAU802186	PSY102165	37%	99.4%	99.1%
SAU802186	SAU802186	100%	100%	100%
SAU802186	SEP202019	65%	100%	99.7%
SAU802186	SHA102028	69%	100%	99.7%
SAU802186	SMU100802	27%	71.9%	76.1%
SAU802186	VCH100542	27%	92.5%	86.1%
SAU802186	YPS000359	27%	91.9%	89.9%
SAU802187	ABA101379	44%	34.5%	82.7%
SAU802187	BCE113538	43%	98.8%	97.3%
SAU802187	BFU101504	42%	98.8%	97.0%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802187	BMA105219	45%	98.8%	96.5%
SAU802187	EBC101789	47%	74.5%	93.9%
SAU802187	ECO101420	45%	99.1%	89.1%
SAU802187	KPN304015	48%	96.1%	94.2%
SAU802187	MAV106640	39%	100%	98.8%
SAU802187	MBV104295	23%	80.8%	14.5%
SAU802187	MTU403167	23%	80.8%	20.7%
SAU802187	PMU101940	21%	56.2%	78.0%
SAU802187	PAE202195	44%	98.8%	96.8%
SAU802187	PPU103733	43%	99.4%	97.7%
SAU802187	PSY104709	46%	83.8%	99.6%
SAU802187	SPA100754	43%	99.7%	96.3%
SAU802187	STY103772	43%	99.7%	97.7%
SAU802187	SAU802187	100%	100%	100%
SAU802187	SEP202022	72%	99.4%	99.1%
SAU802189	BFU102156	34%	96.0%	75.9%
SAU802189	CAC101421	57%	98.5%	97.3%
SAU802189	EBC104273	32%	97.7%	98.2%
SAU802189	EFM201273	59%	98.9%	99.1%
SAU802189	KPN304023	38%	97.4%	98.0%
SAU802189	LMO102257	38%	97.9%	97.4%
SAU802189	SPA103555	32%	98.9%	98.9%
SAU802189	STY104414	33%	98.9%	98.9%
SAU802189	STM100091	32%	98.9%	98.9%
SAU802189	SAU802189	100%	100%	100%
SAU802189	SEP202028	93%	100%	100%
SAU802189	SHA102024	91%	99.6%	99.8%
SAU802189	SMU100441	82%	99.8%	98.7%
SAU802189	SPN401068	81%	99.8%	99.8%
SAU802189	SPY201475	83%	100%	100%
SAU802190	BAN109819	30%	70.4%	95.7%
SAU802190	BAN102068	32%	72.1%	95.3%
SAU802190	CAC103704	53%	98.6%	98.8%
SAU802190	CBO100029	30%	70.2%	90.9%
SAU802190	CDF101451	31%	73.3%	95.9%
SAU802190	EBC100969	35%	71.6%	95.4%
SAU802190	EFA201919	32%	74.7%	99.3%
SAU802190	EFM200856	55%	99.6%	100%
SAU802190	ECO101705	26%	75.8%	99.8%
SAU802190	KPN307137	33%	74.4%	95.5%
SAU802190	LPN103127	29%	10%	9.9%
SAU802190	LMO102762	28%	73.0%	95.7%
SAU802190	PRT105426	24%	69.1%	98.1%
SAU802190	SPA103123	26%	75.8%	99.8%
SAU802190	STY101186	26%	75.8%	99.8%
SAU802190	STM103427	26%	75.8%	99.8%
SAU802190	SAU802190	100%	100%	100%
SAU802190	SEP202030	80%	99.8%	100%
SAU802190	SHA102023	82%	98.6%	100%
SAU802190	SMU100447	76%	99.8%	100%
SAU802190	SPN401069	73%	99.6%	100%
SAU802190	SPY201476	75%	99.8%	100%
SAU802190	VCH101263	33%	73.5%	93.9%
SAU802190	YPS001429	25%	75.6%	98.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802191	BAN110520	38%	89.3%	86.0%
SAU802191	BAN108150	38%	89.3%	86.8%
SAU802191	BAN100622	41%	82.5%	97.7%
SAU802191	BAN112662	39%	89.3%	86.0%
SAU802191	BAN106129	36%	96.1%	94.3%
SAU802191	CAC103163	54%	99.0%	98.1%
SAU802191	CBO103254	42%	87.4%	91.8%
SAU802191	CDF101623	36%	79.6%	70.1%
SAU802191	CDF101453	43%	95.1%	93.1%
SAU802191	EBC103915	33%	96.1%	94.3%
SAU802191	EFA202140	37%	87.4%	84.9%
SAU802191	EFM201537	45%	99.0%	97.1%
SAU802191	ECO101704	34%	96.1%	85.3%
SAU802191	KPN306848	43%	94.2%	91.3%
SAU802191	LMO102156	40%	86.4%	89%
SAU802191	PRT104730	32%	96.1%	86.1%
SAU802191	SPA103124	32%	96.1%	86.1%
SAU802191	STY101178	31%	96.1%	86.1%
SAU802191	STM103428	32%	96.1%	86.1%
SAU802191	SAU802191	100%	100%	100%
SAU802191	SEP202032	74%	100%	99.0%
SAU802191	SHA102022	82%	99.0%	98.1%
SAU802191	SMU100449	75%	100%	99.0%
SAU802191	SPN401070	82%	100%	98.1%
SAU802191	SPY201477	76%	100%	98.1%
SAU802191	VCH101264	34%	94.2%	87.4%
SAU802191	YPS001431	34%	87.4%	78.3%
SAU802192	ABA105994	27%	29.1%	41.8%
SAU802192	BMA106286	27%	38.3%	13.2%
SAU802192	EFA200527	64%	96.9%	95.2%
SAU802192	EFM200718	60%	98.8%	97.0%
SAU802192	ECO103787	24%	84.7%	87.7%
SAU802192	LMO100537	55%	96.9%	93.2%
SAU802192	PAE202357	26%	31.3%	27.7%
SAU802192	PAE202352	34%	18.7%	16.0%
SAU802192	PPU105679	32%	18.7%	16.3%
SAU802192	PSY104152	31%	18.7%	16.3%
SAU802192	SPA103925	25%	84.7%	87.7%
SAU802192	STY103378	25%	84.7%	87.7%
SAU802192	SAU802192	100%	100%	100%
SAU802192	SEP202034	90%	99.7%	100%
SAU802192	SHA102021	91%	99.7%	100%
SAU802192	SMU101449	72%	99.7%	98.8%
SAU802192	SPN401072	75%	99.7%	99.7%
SAU802192	SPY201309	70%	95.1%	95.4%
SAU802192	SPY201478	73%	98.8%	98.2%
SAU802194	BAN108863	32%	84.8%	98.6%
SAU802194	BFR11814	33%	79.5%	94.4%
SAU802194	BMA104191	30%	90.6%	96.3%
SAU802194	CJU100855	34%	74.9%	86.9%
SAU802194	CAC100548	62%	98.8%	98.3%
SAU802194	CBO103215	43%	80.1%	94.5%
SAU802194	CDF103094	39%	86.5%	99.3%
SAU802194	CDF102622	39%	84.8%	96.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802194	CDP101246	39%	70.8%	84.7%
SAU802194	EFA200479	74%	100%	100%
SAU802194	ECO103984	38%	80.7%	92.6%
SAU802194	KPN204541	33%	86.0%	96.7%
SAU802194	LMO101140	40%	83.0%	97.3%
SAU802194	MAV102295	31%	90.1%	96.2%
SAU802194	MBV101530	33%	86.5%	93.7%
SAU802194	MLP100915	32%	90.1%	94.4%
SAU802194	MTU202429	33%	86.5%	92.0%
SAU802194	PMU101645	34%	85.4%	96.0%
SAU802194	PRT105715	26%	73.7%	78.5%
SAU802194	SAU802194	100%	100%	100%
SAU802194	SEP202038	82%	100%	100%
SAU802194	SHA102019	81%	100%	100%
SAU802194	SMU100454	80%	100%	100%
SAU802194	SPN401074	84%	100%	100%
SAU802194	SPY201310	84%	100%	100%
SAU802194	UUR100004	34%	86.5%	98.1%
SAU802194	YPS000070	34%	87.7%	99.3%
SAU802195	CAC101036	47%	99.3%	99.3%
SAU802195	EFA200477	60%	99.3%	99.3%
SAU802195	HPY100567	30%	97.2%	91.4%
SAU802195	KPN100143	29%	45.1%	87.7%
SAU802195	MGE100408	33%	95.8%	92.1%
SAU802195	MPN100247	32%	93.7%	89.5%
SAU802195	SAU802195	100%	100%	100%
SAU802195	SEP202039	78%	100%	100%
SAU802195	SHA102018	78%	100%	100%
SAU802195	SMU100455	76%	100%	100%
SAU802195	SPN401075	74%	99.3%	99.3%
SAU802195	SPY201481	73%	100%	100%
SAU802199	SAU802199	100%	100%	100%
SAU802200	BFR100129	38%	85.8%	91.7%
SAU802200	ECO200334	42%	95.0%	93.5%
SAU802200	KPN302330	40%	95.0%	94.5%
SAU802200	LPN102510	25%	80.1%	90.6%
SAU802200	LPN102953	28%	82.6%	91.8%
SAU802200	LMO101510	64%	100%	100%
SAU802200	SPA104129	40%	95.0%	94.5%
SAU802200	STY103649	41%	96.8%	96.9%
SAU802200	SAU802200	100%	100%	100%
SAU802200	SMU100871	51%	98.2%	99.3%
SAU802200	SPN401331	42%	90.8%	95%
SAU802200	YPS002514	56%	100%	95.3%
SAU802206	BAN105885	29%	99.1%	96.7%
SAU802206	BAN112573	36%	99.1%	92.1%
SAU802206	CAC103299	32%	99.1%	96.6%
SAU802206	CDP101034	33%	99.1%	94.3%
SAU802206	EFA200693	51%	98.3%	97.9%
SAU802206	EFM200265	53%	98.7%	98.3%
SAU802206	LMO101689	41%	99.1%	97.1%
SAU802206	PRT100919	32%	98.3%	82.7%
SAU802206	SAU802206	100%	100%	100%
SAU802206	SEP201253	81%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802206	SHA101838	77%	100%	100%
SAU802207	BAN108476	45%	98.7%	99.6%
SAU802207	BAN112629	56%	99.3%	97.9%
SAU802207	BCE111852	29%	89.7%	93.2%
SAU802207	BFU107623	31%	96.4%	96.9%
SAU802207	BMA102225	30%	96.4%	96.9%
SAU802207	CAC100215	35%	98.0%	95.4%
SAU802207	EBC100415	48%	53.4%	97.0%
SAU802207	EFA200703	64%	98.0%	98.5%
SAU802207	EFM202328	65%	99.8%	99.8%
SAU802207	KPN304223	45%	49.6%	95.9%
SAU802207	LMO102636	56%	98.7%	97.0%
SAU802207	MAV102134	29%	97.7%	94.7%
SAU802207	PRT100920	46%	96.8%	96.6%
SAU802207	PAE204177	32%	96.9%	97.3%
SAU802207	PPU111700	32%	97.8%	98.2%
SAU802207	PPU108615	32%	97.8%	98.2%
SAU802207	SAU802207	100%	100%	100%
SAU802207	SEP201255	87%	100%	100%
SAU802207	SHA101837	84%	100%	100%
SAU802207	SMU100357	62%	99.5%	99.1%
SAU802207	VCH101566	43%	97.1%	94.9%
SAU802217	ABA100673	49%	94.6%	96.1%
SAU802217	BAN112009	71%	100%	100%
SAU802217	BAN109246	73%	100%	100%
SAU802217	BFR11427	50%	93.1%	94.5%
SAU802217	BPT102858	51%	94.6%	94.6%
SAU802217	BBU100337	54%	94.6%	90.4%
SAU802217	BCE104886	50%	94.6%	94.6%
SAU802217	BFU103523	48%	94.6%	94.6%
SAU802217	BMA104857	49%	94.6%	94.6%
SAU802217	CJU101395	48%	93.8%	95.3%
SAU802217	CPN200506	51%	93.8%	91.8%
SAU802217	CTR200396	45%	93.8%	91.7%
SAU802217	CAC102494	68%	100%	100%
SAU802217	CBO103462	70%	100%	100%
SAU802217	CDF100063	66%	100%	100%
SAU802217	CDP100047	47%	93.1%	68.4%
SAU802217	EBC102179	50%	100%	100%
SAU802217	EFA200812	72%	100%	100%
SAU802217	EFM201820	73%	100%	100%
SAU802217	ECO103160	50%	100%	100%
SAU802217	HIN101411	49%	100%	100%
SAU802217	HPY100081	45%	93.8%	95.3%
SAU802217	KPN302005	50%	100%	100%
SAU802217	LPN102542	46%	96.9%	96.5%
SAU802217	LMO100441	73%	100%	100%
SAU802217	MCA100086	52%	94.6%	96.1%
SAU802217	MAV103416	50%	93.1%	72.9%
SAU802217	MBV101153	49%	93.1%	80.1%
SAU802217	MLP100233	52%	93.1%	79.1%
SAU802217	MTU203395	49%	93.1%	80.1%
SAU802217	MGE100427	50%	100%	100%
SAU802217	MPN100226	56%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802217	NGO102668	54%	96.2%	96.2%
SAU802217	NME200353	54%	96.2%	96.2%
SAU802217	PMU100521	52%	100%	100%
SAU802217	PRT100490	51%	100%	100%
SAU802217	PAE204430	50%	100%	100%
SAU802217	PPU105982	51%	100%	100%
SAU802217	PSY108021	50%	100%	100%
SAU802217	SPA100957	50%	100%	100%
SAU802217	STY101559	50%	100%	100%
SAU802217	SAU802217	100%	100%	100%
SAU802217	SEP202046	96%	100%	100%
SAU802217	SHA100041	98%	100%	100%
SAU802217	SMU101370	71%	100%	100%
SAU802217	SPN400272	70%	100%	100%
SAU802217	SPY201485	71%	100%	100%
SAU802217	TPA101014	55%	94.6%	95.3%
SAU802217	UUR100583	55%	97.7%	95.5%
SAU802217	VCH100561	50%	100%	100%
SAU802217	YPS002276	52%	100%	100%
SAU802218	ABA100676	53%	94.5%	96.5%
SAU802218	BAN101291	69%	100%	100%
SAU802218	BAN111521	69%	100%	100%
SAU802218	BFR11426	44%	97.2%	93.5%
SAU802218	BPT102861	52%	96.6%	98.6%
SAU802218	BBU100338	48%	93.1%	92.5%
SAU802218	BCE107311	54%	97.2%	80.1%
SAU802218	BFU103522	55%	97.2%	99.3%
SAU802218	BMA107182	55%	97.2%	78.8%
SAU802218	CJU101396	53%	91.7%	95.0%
SAU802218	CPN200505	48%	93.8%	91.9%
SAU802218	CTR200395	50%	89.0%	86.7%
SAU802218	CAC102148	48%	97.9%	98.6%
SAU802218	CBO103121	52%	99.3%	99.3%
SAU802218	CDF100062	46%	94.5%	95.8%
SAU802218	CDP100045	49%	97.2%	95.9%
SAU802218	EBC102180	58%	94.5%	96.5%
SAU802218	EFA200811	69%	95.2%	94.5%
SAU802218	EFM201491	69%	95.9%	79.0%
SAU802218	ECO103161	58%	94.5%	96.5%
SAU802218	HIN101412	56%	94.5%	96.5%
SAU802218	HPY100082	47%	91.7%	94.3%
SAU802218	KPN301994	56%	94.5%	96.5%
SAU802218	LPN102178	51%	97.2%	97.9%
SAU802218	LMO100177	70%	100%	100%
SAU802218	MCA103453	53%	98.6%	100%
SAU802218	MAV103415	48%	97.2%	95.9%
SAU802218	MBV101152	50%	97.2%	72.3%
SAU802218	MLP100232	46%	97.2%	95.9%
SAU802218	MTU203396	50%	97.2%	95.9%
SAU802218	MGE100428	38%	95.2%	95.9%
SAU802218	MPN100225	40%	95.2%	95.9%
SAU802218	NGO101071	55%	97.9%	99.3%
SAU802218	NME200352	55%	97.9%	99.3%
SAU802218	PMU100520	56%	94.5%	96.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802218	PRT100489	59%	94.5%	96.5%
SAU802218	PAE204431	55%	97.2%	99.3%
SAU802218	PPU105984	54%	97.2%	99.3%
SAU802218	PSY103838	58%	93.8%	95.8%
SAU802218	SPA100958	58%	94.5%	96.5%
SAU802218	STY101563	58%	94.5%	96.5%
SAU802218	SAU802218	100%	100%	100%
SAU802218	SEP202048	93%	100%	100%
SAU802218	SHA100040	89%	77.2%	100%
SAU802218	SMU101369	59%	99.3%	97.3%
SAU802218	SPN400271	64%	99.3%	97.3%
SAU802218	SPY201486	64%	99.3%	97.3%
SAU802218	TPA101015	46%	93.8%	95.8%
SAU802218	UUR100584	48%	90.3%	88.5%
SAU802218	VCH100560	57%	94.5%	96.5%
SAU802218	YPS002279	56%	94.5%	96.5%
SAU802221	BAN100298	34%	90.2%	97.1%
SAU802221	BAN111331	41%	95.5%	93.2%
SAU802221	CAC101129	31%	85.0%	99.2%
SAU802221	CAC103558	35%	87.8%	87.1%
SAU802221	CAC102762	38%	95.8%	95.5%
SAU802221	CBO103078	39%	99.7%	98.6%
SAU802221	CDF103575	38%	97.9%	97.2%
SAU802221	EFA201971	46%	90.6%	92.0%
SAU802221	EFM200592	43%	90.9%	90.0%
SAU802221	LMO100639	43%	94.8%	94.1%
SAU802221	MGE100183	39%	87.4%	82.2%
SAU802221	MPN100637	39%	87.4%	82.5%
SAU802221	SAU802221	100%	100%	100%
SAU802221	SEP202054	63%	100%	100%
SAU802221	SHA102409	44%	19.9%	92.1%
SAU802221	SHA103167	63%	14.3%	100%
SAU802221	SHA100340	65%	100%	100%
SAU802221	SMU101386	44%	97.9%	99.3%
SAU802221	SPN402022	44%	87.4%	89.2%
SAU802221	SPY201677	45%	88.5%	90%
SAU802221	UUR100544	43%	2.8%	30.0%
SAU802222	BAN102912	37%	92.6%	90.1%
SAU802222	BAN100224	50%	96.3%	88.3%
SAU802222	CAC103684	42%	89.2%	87.2%
SAU802222	CBO102095	42%	98.5%	97.2%
SAU802222	CDF103552	42%	92.6%	91.0%
SAU802222	EFA201972	52%	97.8%	96.4%
SAU802222	EFM200542	50%	97.8%	96.4%
SAU802222	KPN102440	34%	89.2%	90.2%
SAU802222	LMO101349	50%	98.1%	96.4%
SAU802222	MGE100182	43%	98.9%	96.0%
SAU802222	MPN100638	42%	99.3%	96.4%
SAU802222	SPA101594	32%	89.2%	88.6%
SAU802222	SAU802222	100%	100%	100%
SAU802222	SEP202056	63%	100%	100%
SAU802222	SHA101370	64%	69.9%	100%
SAU802222	SMU101388	47%	92.9%	86.6%
SAU802222	SPN402023	47%	98.1%	97.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802222	SPY201678	44%	100%	92.9%
SAU802222	UUR100545	47%	94.1%	85.7%
SAU802223	ABA100130	47%	96.7%	86.4%
SAU802223	BAN103288	73%	100%	100%
SAU802223	BAN102478	73%	100%	100%
SAU802223	BFR100896	43%	98.4%	68.3%
SAU802223	BPT100897	50%	99.2%	84.7%
SAU802223	BBU100502	36%	100%	91.1%
SAU802223	BCE109774	47%	99.2%	84.7%
SAU802223	BFU101597	48%	99.2%	85.4%
SAU802223	BMA104335	48%	99.2%	84.7%
SAU802223	CJU101502	45%	99.2%	94.9%
SAU802223	CPN200120	41%	96.7%	93.0%
SAU802223	CTR200782	40%	96.7%	93.0%
SAU802223	CAC100809	57%	99.2%	97.4%
SAU802223	CBO102497	59%	99.2%	98.2%
SAU802223	CDF102169	50%	98.4%	97.3%
SAU802223	CDP100024	44%	96.7%	68.8%
SAU802223	EBC103646	47%	97.5%	85.8%
SAU802223	EFA201974	65%	100%	99.2%
SAU802223	EFM201685	69%	100%	100%
SAU802223	ECO103217	47%	97.5%	85.8%
SAU802223	HIN100784	48%	97.5%	85.2%
SAU802223	HPY101274	46%	99.2%	95.7%
SAU802223	KPN300813	47%	97.5%	85.2%
SAU802223	LMO100340	66%	100%	100%
SAU802223	MCA100427	45%	96.7%	90.8%
SAU802223	MAV101006	44%	96.7%	74.0%
SAU802223	MBV100492	44%	96.7%	60%
SAU802223	MLP101193	42%	96.7%	63.5%
SAU802223	MTU203409	44%	96.7%	60%
SAU802223	MGE100181	35%	96.7%	92.7%
SAU802223	MPN100639	36%	95.9%	91.1%
SAU802223	NGO100883	50%	99.2%	91.0%
SAU802223	NME200096	49%	99.2%	91.0%
SAU802223	PMU101389	47%	97.5%	84.5%
SAU802223	PRT101773	46%	97.5%	85.2%
SAU802223	PAE204235	45%	97.5%	84.5%
SAU802223	PPU104535	47%	97.5%	85.2%
SAU802223	PSY105785	47%	97.5%	85.2%
SAU802223	SPA104312	47%	97.5%	85.8%
SAU802223	STY101829	47%	97.5%	85.8%
SAU802223	SAU802223	100%	100%	100%
SAU802223	SEP202058	95%	100%	100%
SAU802223	SHA100503	98%	100%	99.2%
SAU802223	SMU100584	65%	100%	100%
SAU802223	SPN400216	67%	100%	100%
SAU802223	SPY101855	67%	100%	100%
SAU802223	TPA100211	41%	99.2%	67.7%
SAU802223	UUR100260	41%	96.7%	95.8%
SAU802223	VCH102533	47%	97.5%	85.2%
SAU802223	YPS002494	47%	97.5%	84.5%
SAU802224	ABA100129	41%	93.3%	87.8%
SAU802224	BAN107601	56%	99.7%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802224	BAN108468	78%	100%	100%
SAU802224	BFR10426	41%	98.1%	95.2%
SAU802224	BPT100896	41%	97.1%	93.3%
SAU802224	BBU100501	40%	97.8%	91.9%
SAU802224	BCE103299	40%	97.1%	93.8%
SAU802224	BFU101596	40%	97.1%	93.8%
SAU802224	BMA100053	41%	97.1%	93.8%
SAU802224	CJU101501	34%	94.6%	87.5%
SAU802224	CPN200119	39%	93.0%	79.8%
SAU802224	CTR200783	37%	93.0%	79.2%
SAU802224	CAC100456	62%	100%	99.7%
SAU802224	CBO100600	63%	100%	99.7%
SAU802224	CDF104551	63%	100%	99.1%
SAU802224	CDP100022	47%	93.9%	87.0%
SAU802224	EBC103650	42%	98.1%	93.6%
SAU802224	EFA201975	71%	100%	100%
SAU802224	EFM200465	70%	100%	100%
SAU802224	ECO103218	42%	98.1%	93.6%
SAU802224	HIN100783	42%	98.1%	93.6%
SAU802224	HPY101275	35%	91.1%	84.6%
SAU802224	KPN300703	44%	76.4%	95.7%
SAU802224	LMO100649	75%	100%	100%
SAU802224	MCA100426	45%	93.3%	88.0%
SAU802224	MAV101008	50%	92.4%	83.6%
SAU802224	MBV100494	48%	92.4%	83.6%
SAU802224	MLP101194	48%	92.4%	83.6%
SAU802224	MTU203410	48%	92.4%	83.6%
SAU802224	MGE100180	37%	93.0%	93.0%
SAU802224	MPN100640	34%	96.8%	96.9%
SAU802224	NGO100885	39%	98.1%	93.6%
SAU802224	NME200097	39%	98.1%	93.6%
SAU802224	PMU101390	42%	98.1%	93.6%
SAU802224	PRT101775	42%	98.1%	93.6%
SAU802224	PAE204236	42%	98.1%	92.2%
SAU802224	PPU104534	42%	98.1%	92.2%
SAU802224	PSY100281	40%	46.2%	86.6%
SAU802224	SPA104314	42%	98.1%	93.6%
SAU802224	STY101828	42%	98.1%	93.6%
SAU802224	SAU802224	100%	100%	100%
SAU802224	SEP202059	98%	100%	100%
SAU802224	SHA100502	98%	100%	100%
SAU802224	SMU100586	57%	99.7%	99.7%
SAU802224	SPN400215	58%	99.0%	99.4%
SAU802224	SPY200063	57%	99.7%	99.7%
SAU802224	TPA100210	36%	98.7%	91.5%
SAU802224	UUR100259	40%	95.2%	95.4%
SAU802224	VCH102534	42%	98.1%	93.6%
SAU802224	YPS002493	42%	98.1%	93.6%
SAU802225	ABA100127	60%	97.7%	98.4%
SAU802225	BAN102381	81%	100%	100%
SAU802225	BAN110714	86%	100%	100%
SAU802225	BFR10424	58%	100%	100%
SAU802225	BPT100894	64%	93.8%	91.0%
SAU802225	BBU100500	55%	99.2%	95.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802225	BCE109619	63%	93.8%	91.0%
SAU802225	BFU101594	65%	93.8%	90.3%
SAU802225	BMA109746	64%	93.8%	91.0%
SAU802225	CJU101499	59%	100%	100%
SAU802225	CPN200118	62%	99.2%	96.2%
SAU802225	CTR200784	64%	93.8%	91.7%
SAU802225	CAC100574	77%	98.4%	96.9%
SAU802225	CBO101814	76%	95.3%	93.2%
SAU802225	CDF101597	75%	98.4%	97.0%
SAU802225	CDP100018	67%	95.3%	91.8%
SAU802225	EBC103656	62%	100%	100%
SAU802225	EFA201976	85%	100%	100%
SAU802225	EFM200112	83%	100%	100%
SAU802225	ECO103220	62%	100%	100%
SAU802225	HIN100781	63%	100%	100%
SAU802225	HPY101277	60%	100%	100%
SAU802225	KPN300701	62%	100%	100%
SAU802225	LMO102707	84%	100%	100%
SAU802225	MCA100424	60%	100%	100%
SAU802225	MAV101012	66%	98.4%	92.0%
SAU802225	MBV100327	66%	99.2%	92.1%
SAU802225	MLP101196	66%	98.4%	92.0%
SAU802225	MTU203412	67%	99.2%	92.1%
SAU802225	MGE100179	41%	87.6%	86.3%
SAU802225	MPN100641	47%	92.2%	98.3%
SAU802225	NGO100889	60%	93.8%	92.4%
SAU802225	NME200099	60%	93.8%	92.4%
SAU802225	PMU101392	64%	100%	100%
SAU802225	PRT105644	62%	100%	100%
SAU802225	PAE204238	61%	100%	100%
SAU802225	PPU104532	62%	100%	100%
SAU802225	PSY106472	61%	100%	100%
SAU802225	SPA104318	60%	99.2%	100%
SAU802225	STY101826	62%	100%	100%
SAU802225	SAU802225	100%	100%	100%
SAU802225	SEP200240	99%	100%	100%
SAU802225	SHA100501	100%	100%	100%
SAU802225	SMU100588	84%	95.3%	96.9%
SAU802225	SPN400214	84%	95.3%	96.9%
SAU802225	SPY200062	85%	95.3%	96.9%
SAU802225	TPA100209	61%	96.1%	98.4%
SAU802225	UUR100258	56%	92.2%	98.3%
SAU802225	VCH102536	62%	100%	100%
SAU802225	YPS002491	62%	100%	100%
SAU802226	ABA100126	57%	95.9%	97.5%
SAU802226	BAN113421	85%	33.9%	100%
SAU802226	BAN112977	78%	100%	100%
SAU802226	BFR10423	66%	98.3%	95.2%
SAU802226	BPT100893	58%	100%	100%
SAU802226	BBU100499	55%	99.2%	96.8%
SAU802226	BCE106205	54%	100%	100%
SAU802226	BFU100384	55%	100%	100%
SAU802226	BMA110016	54%	100%	100%
SAU802226	CJU101498	59%	98.3%	99.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802226	CPN200117	54%	100%	100%
SAU802226	CTR200785	53%	100%	100%
SAU802226	CAC101837	66%	100%	99.2%
SAU802226	CBO102219	67%	100%	99.2%
SAU802226	CDF103596	65%	100%	99.2%
SAU802226	CDP100016	59%	100%	100%
SAU802226	EBC103659	53%	95.9%	98.3%
SAU802226	EFA201977	75%	100%	100%
SAU802226	EFM200415	75%	100%	100%
SAU802226	ECO103221	53%	95.9%	98.3%
SAU802226	HIN100780	51%	99.2%	98.4%
SAU802226	HPY101278	58%	98.3%	100%
SAU802226	KPN300700	51%	81.8%	98.0%
SAU802226	LMO102428	78%	100%	100%
SAU802226	MCA100423	58%	95.9%	98.3%
SAU802226	MAV101014	57%	100%	98.4%
SAU802226	MBV100329	54%	100%	98.4%
SAU802226	MLP101197	59%	100%	98.4%
SAU802226	MTU203413	54%	100%	98.4%
SAU802226	MGE100178	65%	99.2%	96.8%
SAU802226	MPN100642	65%	99.2%	96.8%
SAU802226	NGO100891	58%	99.2%	100%
SAU802226	NME200100	58%	99.2%	100%
SAU802226	PMU101393	55%	95.9%	98.3%
SAU802226	PRT100020	52%	88.4%	98.2%
SAU802226	PAE204239	60%	95.9%	98.3%
SAU802226	PPU104531	59%	95.9%	98.3%
SAU802226	PSY105783	60%	60.3%	96.1%
SAU802226	SPA104321	52%	95.9%	98.3%
SAU802226	STY101825	52%	95.9%	98.3%
SAU802226	SAU802226	100%	100%	100%
SAU802226	SEP200241	95%	100%	100%
SAU802226	SHA100500	95%	100%	100%
SAU802226	SMU100590	74%	100%	100%
SAU802226	SPN400213	73%	100%	100%
SAU802226	SPY200061	73%	100%	100%
SAU802226	TPA100208	61%	100%	100%
SAU802226	UUR100257	65%	99.2%	97.0%
SAU802226	VCH102537	53%	95.9%	98.3%
SAU802226	YPS002490	54%	95.9%	98.3%
SAU802227	ABA100104	63%	100%	100%
SAU802227	BPT104512	70%	100%	100%
SAU802227	BBU100498	80%	97.3%	92.3%
SAU802227	BCE112105	68%	100%	100%
SAU802227	BFU103878	68%	100%	100%
SAU802227	BMA103855	68%	100%	100%
SAU802227	CJU101497	78%	100%	100%
SAU802227	CAC101480	97%	100%	100%
SAU802227	CBO103541	94%	100%	97.4%
SAU802227	CDF103770	97%	100%	100%
SAU802227	EBC103975	52%	64.9%	54.3%
SAU802227	EFA203137	84%	100%	100%
SAU802227	EFM202440	84%	100%	100%
SAU802227	ECO103222	63%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802227	HIN100779	64%	100%	100%
SAU802227	HPY101279	70%	100%	100%
SAU802227	KPN202806	52%	64.9%	54.3%
SAU802227	LMO101459	91%	100%	100%
SAU802227	MCA102164	42%	86.5%	71.7%
SAU802227	MBV104764	72%	100%	100%
SAU802227	MLP101198	70%	100%	100%
SAU802227	MTU203414	72%	100%	100%
SAU802227	MGE100177	67%	100%	100%
SAU802227	MPN100643	70%	100%	100%
SAU802227	NGO101308	42%	97.3%	97.6%
SAU802227	NME200101	59%	100%	100%
SAU802227	PMU101394	64%	100%	100%
SAU802227	PRT103159	63%	100%	100%
SAU802227	PAE204240	63%	100%	100%
SAU802227	PSY103480	63%	100%	67.9%
SAU802227	SPA100818	52%	64.9%	54.3%
SAU802227	STY104823	63%	100%	100%
SAU802227	STM104443	52%	64.9%	54.3%
SAU802227	SAU802227	100%	100%	100%
SAU802227	SEP202480	97%	100%	100%
SAU802227	SHA100499	97%	100%	100%
SAU802227	SMU100592	84%	100%	100%
SAU802227	SPN400212	84%	100%	100%
SAU802227	SPY200060	84%	100%	100%
SAU802227	TPA100207	72%	100%	100%
SAU802227	UUR100256	70%	100%	100%
SAU802227	VCH102538	75%	100%	100%
SAU802227	YPS003891	65%	100%	100%
SAU802228	ABA102422	69%	94.4%	93.2%
SAU802228	BAN103338	88%	59.7%	100%
SAU802228	BFR100583	70%	100%	100%
SAU802228	BPT100892	68%	100%	100%
SAU802228	BBU100168	62%	97.2%	77.8%
SAU802228	BCE109557	66%	100%	100%
SAU802228	BFU100382	66%	100%	94.7%
SAU802228	BMA107769	65%	100%	100%
SAU802228	CJU101496	69%	100%	100%
SAU802228	CPN200690	54%	97.2%	95.9%
SAU802228	CTR200589	57%	97.2%	95.9%
SAU802228	CAC103209	77%	100%	100%
SAU802228	CBO100838	77%	100%	100%
SAU802228	CDF104286	80%	100%	100%
SAU802228	CDP100014	69%	100%	100%
SAU802228	EBC100928	72%	97.2%	97.2%
SAU802228	EFA205225	84%	100%	100%
SAU802228	EFM200666	83%	100%	100%
SAU802228	ECO100859	71%	97.2%	97.2%
SAU802228	HIN100527	71%	97.2%	83.3%
SAU802228	HPY101280	59%	100%	100%
SAU802228	KPN301361	70%	86.1%	96.9%
SAU802228	LPN102139	68%	100%	98.6%
SAU802228	LMO101112	83%	100%	100%
SAU802228	MCA100273	72%	97.2%	95.9%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802228	MAV101015	69%	100%	100%
SAU802228	MBV100332	69%	100%	100%
SAU802228	MLP101199	69%	100%	100%
SAU802228	MTU203415	69%	100%	100%
SAU802228	MGE100176	48%	94.4%	97.1%
SAU802228	MPN100644	53%	95.8%	88.5%
SAU802228	NGO100894	67%	97.2%	97.2%
SAU802228	NME200102	67%	97.2%	97.2%
SAU802228	PMU101031	70%	97.2%	97.2%
SAU802228	PRT101847	72%	97.2%	97.2%
SAU802228	PAE202617	71%	97.2%	97.2%
SAU802228	PPU110129	71%	97.2%	97.2%
SAU802228	PSY108380	71%	97.2%	97.2%
SAU802228	SPA101389	71%	97.2%	97.2%
SAU802228	STY102886	71%	97.2%	97.2%
SAU802228	SAU802228	100%	100%	100%
SAU802228	SEP200242	98%	100%	100%
SAU802228	SHA100498	98%	100%	98.6%
SAU802228	SMU100596	83%	100%	100%
SAU802228	SPN400211	81%	100%	80%
SAU802228	SPY200059	81%	100%	100%
SAU802228	TPA100096	58%	97.2%	97.2%
SAU802228	UUR100255	55%	100%	97.3%
SAU802228	VCH101709	75%	97.2%	97.2%
SAU802228	YPS003792	72%	97.2%	97.2%
SAU802229	ABA102578	49%	99.1%	99.5%
SAU802229	BAN108855	54%	98.6%	97.7%
SAU802229	BAN106781	64%	98.6%	97.7%
SAU802229	BFR10586	39%	100%	99.5%
SAU802229	BPT101280	48%	86.5%	83.5%
SAU802229	BBU100416	43%	98.6%	98.1%
SAU802229	BCE114693	54%	86.5%	82.7%
SAU802229	BFU106856	54%	86.5%	82.4%
SAU802229	BMA102106	54%	86.5%	82.7%
SAU802229	CJU100600	28%	97.2%	94.3%
SAU802229	CPN200508	34%	95.8%	94.4%
SAU802229	CTR200398	34%	97.7%	86.2%
SAU802229	CAC102891	53%	100%	100%
SAU802229	CBO103787	53%	98.6%	98.1%
SAU802229	CDF102350	56%	98.6%	95.9%
SAU802229	CDP100003	40%	98.6%	98.9%
SAU802229	EBC103984	47%	98.6%	99.5%
SAU802229	EFA201978	64%	99.1%	99.1%
SAU802229	EFM200623	62%	99.1%	99.5%
SAU802229	ECO100465	47%	98.6%	99.5%
SAU802229	HIN100331	51%	98.6%	99.5%
SAU802229	HPY100611	29%	95.3%	92.7%
SAU802229	KPN303865	47%	98.6%	99.5%
SAU802229	LPN102084	42%	99.1%	99.5%
SAU802229	LMO102187	66%	98.6%	98.6%
SAU802229	MCA101231	47%	98.6%	98.6%
SAU802229	MAV102071	38%	94.9%	94.5%
SAU802229	MBV101628	37%	94.9%	94.5%
SAU802229	MLP101114	35%	94.9%	94.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802229	MTU200730	37%	94.9%	94.5%
SAU802229	MGE100174	36%	89.8%	88.3%
SAU802229	MPN100646	31%	89.8%	88.8%
SAU802229	NGO100911	47%	98.6%	99.1%
SAU802229	NME200954	47%	98.6%	99.1%
SAU802229	PMU100284	50%	98.6%	99.5%
SAU802229	PRT104973	47%	98.6%	99.5%
SAU802229	PAE203684	47%	98.6%	99.5%
SAU802229	PPU107935	49%	98.6%	99.5%
SAU802229	PSY104919	45%	81.9%	97.8%
SAU802229	SPA100230	47%	94.9%	88.3%
SAU802229	STY100842	47%	98.6%	99.5%
SAU802229	STM100555	47%	98.6%	99.5%
SAU802229	SAU802229	100%	100%	100%
SAU802229	SEP200243	91%	100%	100%
SAU802229	SHA100179	91%	100%	99.5%
SAU802229	SMU100597	56%	100%	99.5%
SAU802229	SPN400210	56%	100%	99.5%
SAU802229	SPY200058	57%	96.7%	96.2%
SAU802229	TPA100588	44%	94.9%	94.3%
SAU802229	UUR100253	37%	98.6%	98.1%
SAU802229	VCH100969	49%	98.6%	99.5%
SAU802229	YPS001716	45%	98.6%	99.5%
SAU802230	ABA100105	40%	96.0%	91.6%
SAU802230	BAN100422	54%	54.4%	100%
SAU802230	BAN100831	41%	98.8%	98.6%
SAU802230	BAN109756	56%	99.3%	98.8%
SAU802230	BAN106840	58%	99.3%	99.3%
SAU802230	BFR12413	38%	98.8%	95.1%
SAU802230	BPT100873	39%	96.5%	93.4%
SAU802230	BBU100497	34%	98.6%	96.8%
SAU802230	BCE109015	37%	94.4%	96%
SAU802230	BFU100380	36%	96.0%	92.4%
SAU802230	BMA107419	37%	94.4%	96.0%
SAU802230	CJU101592	40%	96.3%	97.9%
SAU802230	CPN200116	36%	97.9%	95.7%
SAU802230	CTR200786	36%	98.4%	97.2%
SAU802230	CAC102097	36%	99.3%	99.3%
SAU802230	CBO103220	36%	99.3%	99.5%
SAU802230	CDF103985	38%	99.3%	99.5%
SAU802230	CDP100001	39%	97.2%	97.7%
SAU802230	EBC103637	41%	96.0%	93.2%
SAU802230	EFA201979	46%	99.3%	99.3%
SAU802230	EFM200235	48%	99.3%	99.5%
SAU802230	ECO103223	41%	96.0%	93.2%
SAU802230	HIN100778	38%	96.7%	95.9%
SAU802230	HPY101282	38%	96.3%	97.9%
SAU802230	KPN300616	40%	78.4%	95.2%
SAU802230	LPN101432	38%	84.2%	98.1%
SAU802230	LMO101544	54%	99.3%	99.5%
SAU802230	MCA100141	37%	95.8%	92.7%
SAU802230	MAV102070	39%	99.3%	96.9%
SAU802230	MBV101627	39%	99.3%	99.5%
SAU802230	MLP101115	38%	99.3%	99.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802230	MTU200729	39%	99.3%	99.5%
SAU802230	MGE100173	35%	98.4%	90.1%
SAU802230	MPN100647	35%	98.4%	89.7%
SAU802230	NGO100896	38%	95.8%	93.3%
SAU802230	NME200103	38%	95.8%	93.3%
SAU802230	PMU101395	39%	97.2%	96.4%
SAU802230	PRT100105	39%	47.0%	95.3%
SAU802230	PAE204241	38%	96.0%	92.5%
SAU802230	PPU112340	37%	97.0%	95.3%
SAU802230	PSY100299	37%	97.0%	95.0%
SAU802230	SPA104324	41%	94.0%	94.4%
SAU802230	STY101824	40%	96.0%	93.2%
SAU802230	SAU802230	100%	100%	100%
SAU802230	SEP200245	89%	100%	100%
SAU802230	SHA100178	82%	86.0%	100%
SAU802230	SMU100598	45%	98.4%	97.7%
SAU802230	SPN400209	47%	97.9%	97.2%
SAU802230	SPY200057	46%	99.1%	98.4%
SAU802230	TPA100206	35%	98.1%	93.8%
SAU802230	UUR100252	33%	97.7%	91.7%
SAU802230	VCH102539	38%	96.0%	93.2%
SAU802230	YPS002488	40%	96.0%	93.2%
SAU802231	ABA100106	45%	98.6%	97.9%
SAU802231	BAN100388	59%	100%	100%
SAU802231	BAN101282	76%	100%	100%
SAU802231	BFR100671	50%	96.6%	96.6%
SAU802231	BPT100871	47%	97.3%	96.6%
SAU802231	BBU100496	51%	89.7%	90.3%
SAU802231	BCE108533	46%	97.3%	97.9%
SAU802231	BFU100391	47%	97.3%	97.9%
SAU802231	BMA101533	47%	97.3%	97.9%
SAU802231	CJU101593	35%	88.4%	98.5%
SAU802231	CPN200115	34%	81.5%	84.0%
SAU802231	CTR200787	41%	84.9%	87.5%
SAU802231	CAC101804	66%	100%	100%
SAU802231	CBO103582	71%	100%	100%
SAU802231	CDF100735	62%	100%	98%
SAU802231	CDP101730	50%	97.3%	94.6%
SAU802231	EBC103640	45%	98.6%	99.3%
SAU802231	EFA201980	78%	100%	100%
SAU802231	EFM201975	77%	100%	100%
SAU802231	ECO103224	46%	98.6%	99.3%
SAU802231	HIN100777	45%	98.6%	99.3%
SAU802231	HPY101283	39%	89.7%	96.3%
SAU802231	KPN300615	44%	95.2%	99.3%
SAU802231	LPN100259	40%	98.6%	99.3%
SAU802231	LMO102003	82%	100%	100%
SAU802231	MCA100140	43%	98.6%	97.9%
SAU802231	MAV102081	51%	97.3%	95.9%
SAU802231	MBV101609	47%	97.3%	95.9%
SAU802231	MLP101118	48%	97.3%	95.9%
SAU802231	MTU200720	48%	97.3%	95.9%
SAU802231	MGE100172	42%	100%	99.3%
SAU802231	MPN100648	39%	100%	98.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802231	NGO100899	41%	99.3%	100%
SAU802231	NME200104	42%	99.3%	100%
SAU802231	PMU101396	46%	98.6%	99.3%
SAU802231	PRT103332	43%	98.6%	99.3%
SAU802231	PAE204242	42%	98.6%	99.3%
SAU802231	PPU104529	45%	98.6%	99.3%
SAU802231	PSY107337	47%	98.6%	99.3%
SAU802231	SPA104326	47%	98.6%	99.3%
SAU802231	STY101823	47%	98.6%	99.3%
SAU802231	SAU802231	100%	100%	100%
SAU802231	SEP200247	94%	100%	100%
SAU802231	SHA100093	82%	58.9%	100%
SAU802231	SMU100599	80%	100%	100%
SAU802231	SPN400208	83%	100%	100%
SAU802231	SPY200056	78%	100%	100%
SAU802231	TPA100205	46%	97.9%	94.1%
SAU802231	UUR100251	48%	93.2%	92.6%
SAU802231	VCH102540	48%	98.6%	99.3%
SAU802231	YPS002485	45%	98.6%	99.3%
SAU802232	ABA100108	37%	98.3%	100%
SAU802232	BAN104365	76%	94.9%	93.3%
SAU802232	BFR100963	44%	94.9%	96.6%
SAU802232	BPT104115	48%	94.9%	91.8%
SAU802232	BBU100495	32%	93.2%	54.5%
SAU802232	BFU104042	49%	89.8%	84.1%
SAU802232	BMA107387	47%	89.8%	84.1%
SAU802232	CAC103086	52%	96.6%	100%
SAU802232	CBO100965	53%	98.3%	98.3%
SAU802232	CDF102795	62%	98.3%	95.1%
SAU802232	CDP102962	49%	93.2%	90.2%
SAU802232	EBC103644	47%	98.3%	100%
SAU802232	EFA205229	62%	98.3%	98.3%
SAU802232	EFM200795	65%	98.3%	98.3%
SAU802232	ECO103225	50%	98.3%	100%
SAU802232	HIN100776	42%	98.3%	100%
SAU802232	KPN300492	45%	94.9%	100%
SAU802232	LPN102267	51%	94.9%	91.8%
SAU802232	LMO100063	75%	98.3%	98.3%
SAU802232	MCA102911	36%	98.3%	98.3%
SAU802232	MAV102080	48%	94.9%	78.9%
SAU802232	MBV101607	49%	96.6%	87.7%
SAU802232	MLP101119	49%	96.6%	80.3%
SAU802232	MTU200719	49%	96.6%	87.7%
SAU802232	NGO102470	40%	93.2%	90.2%
SAU802232	NME200105	41%	93.2%	90.2%
SAU802232	PMU101397	42%	98.3%	100%
SAU802232	PRT100559	49%	98.3%	96.7%
SAU802232	PAE204243	42%	96.6%	98.3%
SAU802232	PPU108173	40%	96.6%	98.3%
SAU802232	PSY107474	38%	96.6%	98.3%
SAU802232	SPA106249	47%	98.3%	100%
SAU802232	STY105107	47%	98.3%	100%
SAU802232	SAU802232	100%	100%	100%
SAU802232	SEP202555	94%	100%	98.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802232	SHA100092	96%	100%	100%
SAU802232	SMU102834	67%	98.3%	96.7%
SAU802232	SPN400207	68%	98.3%	96.7%
SAU802232	SPY200055	65%	98.3%	96.7%
SAU802232	VCH102541	48%	98.3%	100%
SAU802232	YPS004281	44%	98.3%	100%
SAU802233	ABA100109	53%	95.8%	96.4%
SAU802233	BAN111381	75%	98.8%	99.4%
SAU802233	BAN112822	77%	98.8%	98.8%
SAU802233	BFR10783	52%	94.0%	90.7%
SAU802233	BPT100869	48%	98.2%	95.3%
SAU802233	BBU100494	54%	92.2%	92.7%
SAU802233	BCE102110	48%	75.9%	92.6%
SAU802233	BFU100390	48%	96.4%	93.0%
SAU802233	BMA101481	49%	96.4%	94.7%
SAU802233	CJU101594	58%	84.3%	95.2%
SAU802233	CPN200114	42%	98.2%	98.8%
SAU802233	CTR200788	44%	94.6%	95.8%
SAU802233	CAC100146	64%	97.6%	98.2%
SAU802233	CBO100463	63%	97.6%	98.2%
SAU802233	CDF100733	66%	93.4%	91.7%
SAU802233	CDP101728	59%	97.6%	77.9%
SAU802233	EBC103648	55%	98.8%	98.8%
SAU802233	EFA201981	72%	93.4%	93.4%
SAU802233	EFM200438	72%	93.4%	93.4%
SAU802233	ECO103226	55%	98.8%	98.2%
SAU802233	HIN100775	55%	98.8%	98.8%
SAU802233	HPY101284	62%	86.7%	94.1%
SAU802233	KPN300491	55%	98.8%	98.2%
SAU802233	LPN100995	56%	92.8%	91.7%
SAU802233	LMO101368	78%	93.4%	92.8%
SAU802233	MCA100160	55%	95.8%	96.4%
SAU802233	MAV102079	56%	97.0%	71.6%
SAU802233	MBV101605	57%	97.0%	73.2%
SAU802233	MLP101120	58%	93.4%	71.4%
SAU802233	MTU200718	57%	97.0%	73.2%
SAU802233	MGE100171	50%	93.4%	73.5%
SAU802233	MPN100649	50%	93.4%	70.8%
SAU802233	NGO100919	49%	96.4%	93.0%
SAU802233	NME200106	49%	96.4%	93.0%
SAU802233	PMU101398	56%	98.8%	98.8%
SAU802233	PRT100558	54%	98.8%	98.8%
SAU802233	PAE204244	52%	98.8%	99.4%
SAU802233	PPU104527	49%	99.4%	100%
SAU802233	PSY105833	49%	98.8%	99.4%
SAU802233	SPA104328	56%	98.8%	98.2%
SAU802233	STY101822	55%	98.8%	98.2%
SAU802233	SAU802233	100%	100%	100%
SAU802233	SEP200249	98%	100%	100%
SAU802233	SHA100091	98%	100%	100%
SAU802233	SMU100600	67%	96.4%	97.6%
SAU802233	SPN400206	65%	96.4%	97.6%
SAU802233	SPY200054	67%	96.4%	97.6%
SAU802233	TPA100204	54%	94.6%	91.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802233	UUR100250	53%	97.6%	80.3%
SAU802233	VCH102542	54%	98.8%	98.8%
SAU802233	YPS002482	53%	98.8%	98.2%
SAU802234	ABA100110	46%	95.8%	98.3%
SAU802234	BAN106991	70%	100%	100%
SAU802234	BFR100058	59%	74.8%	100%
SAU802234	BPT100868	42%	96.6%	100%
SAU802234	BBU100493	37%	89.9%	89.9%
SAU802234	BCE113907	44%	96.6%	100%
SAU802234	BFU100389	40%	96.6%	100%
SAU802234	BMA109275	44%	96.6%	100%
SAU802234	CJU101595	43%	93.3%	91.5%
SAU802234	CPN200113	41%	95.0%	94.3%
SAU802234	CTR200789	43%	95.0%	94.3%
SAU802234	CAC102283	60%	96.6%	99.1%
SAU802234	CBO100811	54%	100%	97.5%
SAU802234	CDF103929	58%	100%	100%
SAU802234	CDP101725	54%	91.6%	81.5%
SAU802234	EBC103652	43%	96.6%	100%
SAU802234	EFA201982	68%	100%	100%
SAU802234	EFM200146	70%	100%	100%
SAU802234	ECO103227	45%	96.6%	100%
SAU802234	HIN100774	42%	96.6%	100%
SAU802234	HPY101285	40%	93.3%	90.8%
SAU802234	KPN300490	45%	96.6%	100%
SAU802234	LPN101342	44%	89.9%	98.3%
SAU802234	LMO102391	70%	100%	100%
SAU802234	MCA100159	49%	95.8%	98.3%
SAU802234	MAV102077	50%	91.6%	81.5%
SAU802234	MBV101604	51%	91.6%	90.2%
SAU802234	MLP101121	49%	91.6%	90.9%
SAU802234	MTU200717	51%	91.6%	90.2%
SAU802234	MGE100170	37%	99.2%	100%
SAU802234	MPN100650	37%	95.0%	97.4%
SAU802234	NGO100921	45%	96.6%	100%
SAU802234	NME200107	45%	96.6%	100%
SAU802234	PMU101399	42%	96.6%	100%
SAU802234	PRT100557	45%	96.6%	100%
SAU802234	PAE204245	48%	95.0%	97.4%
SAU802234	PPU104526	47%	95.8%	98.3%
SAU802234	PSY105780	51%	78.2%	95.9%
SAU802234	SPA104494	41%	96.6%	100%
SAU802234	STY101821	45%	96.6%	100%
SAU802234	SAU802234	100%	100%	100%
SAU802234	SEP200251	88%	100%	100%
SAU802234	SHA100055	90%	100%	100%
SAU802234	SMU100601	65%	100%	100%
SAU802234	SPN400205	66%	100%	100%
SAU802234	SPY200053	67%	100%	100%
SAU802234	TPA100203	41%	95.8%	95%
SAU802234	UUR100249	45%	98.3%	95.0%
SAU802234	VCH102543	38%	96.6%	100%
SAU802234	YPS002455	43%	96.6%	100%
SAU802235	ABA100111	44%	98.3%	98.9%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802235	BAN102950	57%	98.3%	99.4%
SAU802235	BAN110172	62%	100%	100%
SAU802235	BFR10781	45%	98.9%	97.9%
SAU802235	BPT100867	41%	98.3%	98.9%
SAU802235	BBU100492	42%	99.4%	98.3%
SAU802235	BCE105068	42%	98.3%	98.9%
SAU802235	BFU100388	43%	98.3%	98.9%
SAU802235	BMA103347	42%	98.3%	98.9%
SAU802235	CJU101596	43%	100%	99.4%
SAU802235	CPN200112	45%	100%	97.8%
SAU802235	CTR200790	44%	100%	97.8%
SAU802235	CAC101071	56%	100%	100%
SAU802235	CBO102597	59%	100%	99.4%
SAU802235	CDF100753	57%	100%	99.4%
SAU802235	CDP101722	55%	100%	100%
SAU802235	EBC103655	44%	98.3%	98.9%
SAU802235	EFA201983	63%	100%	100%
SAU802235	EFM201241	65%	100%	100%
SAU802235	ECO103228	44%	98.3%	98.9%
SAU802235	HIN100773	46%	98.3%	98.9%
SAU802235	HPY101286	42%	100%	99.4%
SAU802235	KPN300489	59%	18.0%	91.4%
SAU802235	LPN100869	45%	98.3%	98.9%
SAU802235	LMO102101	65%	100%	100%
SAU802235	MCA100158	45%	98.3%	98.9%
SAU802235	MAV102075	50%	100%	100%
SAU802235	MBV101643	50%	100%	100%
SAU802235	MLP101122	50%	100%	100%
SAU802235	MTU200716	50%	100%	100%
SAU802235	MGE100169	45%	100%	98.4%
SAU802235	MPN100651	43%	100%	98.4%
SAU802235	NGO100923	44%	98.3%	98.9%
SAU802235	NME200108	43%	98.3%	98.9%
SAU802235	PMU101400	45%	98.3%	98.9%
SAU802235	PRT100556	45%	98.3%	98.9%
SAU802235	PAE204246	43%	98.3%	98.9%
SAU802235	PPU104525	47%	98.3%	98.9%
SAU802235	PSY100295	45%	98.3%	98.9%
SAU802235	SPA104330	44%	98.3%	98.9%
SAU802235	STY101820	44%	98.3%	98.9%
SAU802235	SAU802235	100%	100%	100%
SAU802235	SEP200253	92%	100%	100%
SAU802235	SHA100054	87%	60.1%	100%
SAU802235	SMU100602	60%	100%	100%
SAU802235	SPN400204	58%	100%	100%
SAU802235	SPY200052	61%	100%	100%
SAU802235	TPA100202	45%	99.4%	98.9%
SAU802235	UUR100248	37%	98.9%	97.3%
SAU802235	VCH102544	44%	98.3%	98.9%
SAU802235	YPS002454	44%	98.3%	98.9%
SAU802236	ABA100112	47%	99.2%	99.2%
SAU802236	BAN113611	80%	98.5%	95.6%
SAU802236	BAN101892	79%	100%	100%
SAU802236	BFR10780	52%	98.5%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802236	BPT100866	47%	99.2%	99.2%
SAU802236	BBU100491	43%	100%	100%
SAU802236	BCE101537	49%	99.2%	99.2%
SAU802236	BFU100387	48%	99.2%	99.2%
SAU802236	BMA101128	51%	99.2%	99.2%
SAU802236	CJU101597	41%	98.5%	99.2%
SAU802236	CPN200111	41%	97.7%	97.0%
SAU802236	CTR200791	42%	97.7%	97.0%
SAU802236	CAC102421	62%	100%	100%
SAU802236	CBO102964	63%	100%	100%
SAU802236	CDF100752	68%	100%	100%
SAU802236	CDP101719	59%	100%	100%
SAU802236	EBC103658	51%	99.2%	99.2%
SAU802236	EFA201984	78%	100%	100%
SAU802236	EFM200970	76%	100%	100%
SAU802236	ECO103229	51%	99.2%	99.2%
SAU802236	HIN100772	47%	99.2%	99.2%
SAU802236	HPY101287	43%	98.5%	99.2%
SAU802236	KPN300573	50%	87.1%	98.3%
SAU802236	LPN100471	43%	99.2%	99.2%
SAU802236	LMO100791	78%	100%	100%
SAU802236	MCA100157	46%	99.2%	99.2%
SAU802236	MAV102073	56%	100%	100%
SAU802236	MBV101642	56%	100%	100%
SAU802236	MLP101123	56%	100%	100%
SAU802236	MTU200715	56%	100%	100%
SAU802236	MGE100168	45%	97.0%	92.2%
SAU802236	MPN100652	46%	97.0%	91.5%
SAU802236	NGO100925	48%	99.2%	99.2%
SAU802236	NME200109	48%	99.2%	99.2%
SAU802236	PMU101401	48%	99.2%	99.2%
SAU802236	PRT100555	47%	99.2%	99.2%
SAU802236	PAE204247	43%	100%	100%
SAU802236	PPU108197	44%	100%	100%
SAU802236	PSY108276	43%	100%	100%
SAU802236	SPA104332	51%	99.2%	99.2%
SAU802236	STY101809	51%	99.2%	99.2%
SAU802236	SAU802236	100%	100%	100%
SAU802236	SEP200255	96%	100%	100%
SAU802236	SHA101609	90%	72.7%	100%
SAU802236	SMU100603	72%	100%	100%
SAU802236	SPN400203	75%	100%	100%
SAU802236	SPY200051	78%	100%	100%
SAU802236	TPA100201	50%	100%	100%
SAU802236	UUR100247	46%	97.0%	97.7%
SAU802236	VCH102545	48%	99.2%	99.2%
SAU802236	YPS002453	51%	99.2%	99.2%
SAU802237	BAN104895	83%	100%	100%
SAU802237	BAN100258	83%	100%	100%
SAU802237	BBU100490	52%	100%	82.4%
SAU802237	CJU101598	60%	100%	100%
SAU802237	CAC102855	63%	100%	100%
SAU802237	CBO101206	59%	100%	100%
SAU802237	CDF102552	80%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802237	EFA202953	77%	100%	100%
SAU802237	EFM201806	77%	100%	100%
SAU802237	HPY101288	65%	100%	100%
SAU802237	LMO100535	83%	100%	100%
SAU802237	MAV102072	60%	100%	100%
SAU802237	MBV101641	60%	100%	100%
SAU802237	MLP101124	59%	100%	100%
SAU802237	MTU200714	60%	100%	100%
SAU802237	MGE100167	60%	100%	100%
SAU802237	MPN100653	62%	100%	100%
SAU802237	SAU802237	100%	100%	100%
SAU802237	SEP202534	98%	100%	100%
SAU802237	SHA103188	100%	100%	100%
SAU802237	SMU102003	77%	100%	100%
SAU802237	SPY200050	75%	100%	100%
SAU802237	TPA100200	55%	100%	100%
SAU802237	UUR100246	72%	100%	100%
SAU802238	ABA100107	62%	85.5%	100%
SAU802238	BAN113536	73%	100%	100%
SAU802238	BAN110693	84%	100%	100%
SAU802238	BFR10778	52%	97.8%	94.1%
SAU802238	BPT100865	59%	99.4%	99.4%
SAU802238	BBU100489	58%	97.2%	95.6%
SAU802238	BCE101479	60%	99.4%	99.4%
SAU802238	BFU100385	61%	99.4%	99.4%
SAU802238	BMA102975	61%	99.4%	99.4%
SAU802238	CJU101599	52%	100%	98.9%
SAU802238	CPN200110	49%	100%	98.9%
SAU802238	CTR200792	50%	100%	98.9%
SAU802238	CAC100782	66%	97.8%	97.2%
SAU802238	CBO103765	66%	100%	99.4%
SAU802238	CDF100751	69%	99.4%	98.9%
SAU802238	CDP101582	58%	98.9%	94.7%
SAU802238	EBC103664	60%	100%	100%
SAU802238	EFA201985	83%	100%	100%
SAU802238	EFM200921	82%	100%	100%
SAU802238	ECO103231	60%	100%	100%
SAU802238	HIN100770	60%	100%	100%
SAU802238	HPY101289	49%	98.3%	97.2%
SAU802238	KPN300575	64%	79.3%	100%
SAU802238	LPN102846	56%	41.3%	93.7%
SAU802238	LMO101852	79%	100%	100%
SAU802238	MCA100155	55%	99.4%	100%
SAU802238	MAV102069	56%	98.9%	94.7%
SAU802238	MBV101640	57%	98.9%	94.7%
SAU802238	MLP101125	58%	98.9%	94.7%
SAU802238	MTU200713	57%	98.9%	94.7%
SAU802238	MGE100166	56%	100%	99.4%
SAU802238	MPN100654	56%	100%	99.4%
SAU802238	NGO100929	58%	99.4%	99.4%
SAU802238	NME200111	58%	99.4%	99.4%
SAU802238	PMU101403	60%	100%	100%
SAU802238	PRT100553	60%	100%	94.2%
SAU802238	PAE204249	60%	99.4%	99.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802238	PPU104523	58%	99.4%	99.4%
SAU802238	PSY100243	66%	46.4%	98.8%
SAU802238	SPA104334	60%	100%	100%
SAU802238	STY101807	60%	100%	100%
SAU802238	SAU802238	100%	100%	100%
SAU802238	SEP200260	96%	100%	100%
SAU802238	SHA100780	94%	100%	100%
SAU802238	SMU100604	76%	99.4%	98.9%
SAU802238	SPN400201	76%	99.4%	98.9%
SAU802238	SPY200049	76%	99.4%	98.9%
SAU802238	TPA100199	54%	98.3%	95.1%
SAU802238	UUR100245	57%	98.3%	95.7%
SAU802238	VCH102547	62%	100%	100%
SAU802238	YPS002451	59%	100%	100%
SAU802239	ABA102168	52%	84.8%	96.7%
SAU802239	BAN110382	68%	94.3%	96.1%
SAU802239	BAN104944	71%	94.3%	96.1%
SAU802239	BFR103505	55%	97.1%	97.2%
SAU802239	BPT104094	47%	92.4%	91.5%
SAU802239	BBU100488	39%	94.3%	96.0%
SAU802239	BCE110380	45%	91.4%	92.2%
SAU802239	BFU100383	41%	96.2%	97.1%
SAU802239	BMA108868	47%	91.4%	92.2%
SAU802239	CJU101600	55%	64.8%	88.3%
SAU802239	CPN200109	45%	81.9%	73.9%
SAU802239	CTR200793	47%	78.1%	70.3%
SAU802239	CAC102906	45%	94.3%	94.3%
SAU802239	CBO100250	49%	94.3%	95.2%
SAU802239	CDF103678	55%	96.2%	99.0%
SAU802239	CDP101580	54%	96.2%	100%
SAU802239	EBC103629	53%	95.2%	96.2%
SAU802239	EFA205255	65%	94.3%	96.1%
SAU802239	EFM201757	66%	94.3%	96.1%
SAU802239	ECO103232	53%	95.2%	96.2%
SAU802239	HIN100769	52%	94.3%	96.1%
SAU802239	HPY101290	58%	63.8%	91.8%
SAU802239	KPN305017	53%	95.2%	96.2%
SAU802239	LMO101665	70%	96.2%	98.1%
SAU802239	MCA100154	51%	94.3%	94.3%
SAU802239	MAV102067	49%	96.2%	100%
SAU802239	MBV101639	50%	96.2%	100%
SAU802239	MLP101126	48%	96.2%	100%
SAU802239	MTU200712	50%	96.2%	100%
SAU802239	MGE100165	34%	94.3%	97.2%
SAU802239	MPN100655	36%	94.3%	97.3%
SAU802239	NGO100931	48%	94.3%	95.3%
SAU802239	NME200112	49%	94.3%	95.3%
SAU802239	PMU101404	55%	94.3%	96.1%
SAU802239	PRT103501	47%	34.3%	89.7%
SAU802239	PAE204250	49%	96.2%	97.1%
SAU802239	PPU104522	47%	94.3%	95.2%
SAU802239	PSY100105	47%	94.3%	95.2%
SAU802239	SPA104335	51%	95.2%	96.2%
SAU802239	STY101806	53%	95.2%	96.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802239	SAU802239	100%	100%	100%
SAU802239	SEP200261	94%	100%	100%
SAU802239	SHA101599	92%	67.6%	100%
SAU802239	SMU100605	65%	94.3%	97.0%
SAU802239	SPN400200	68%	94.3%	97.0%
SAU802239	SPY200048	63%	94.3%	97.0%
SAU802239	TPA100198	51%	92.4%	92.2%
SAU802239	UUR100244	48%	97.1%	95.5%
SAU802239	VCH102548	52%	97.1%	96.2%
SAU802239	YPS002450	53%	95.2%	96.2%
SAU802240	ABA102167	65%	91.0%	96.5%
SAU802240	BAN108009	88%	100%	100%
SAU802240	BFR100659	64%	100%	100%
SAU802240	BPT100864	63%	100%	100%
SAU802240	BBU100487	59%	100%	98.4%
SAU802240	BCE113728	68%	100%	100%
SAU802240	BFU100381	68%	100%	100%
SAU802240	BMA101057	67%	100%	100%
SAU802240	CJU101601	68%	100%	100%
SAU802240	CPN200108	63%	100%	100%
SAU802240	CTR200794	64%	100%	100%
SAU802240	CAC101685	73%	100%	100%
SAU802240	CBO100636	77%	100%	100%
SAU802240	CDF102312	81%	100%	100%
SAU802240	CDP101578	75%	100%	100%
SAU802240	EBC103643	67%	100%	100%
SAU802240	EFA201986	90%	100%	100%
SAU802240	EFM201996	91%	100%	100%
SAU802240	ECO103233	66%	100%	100%
SAU802240	HIN100768	69%	100%	100%
SAU802240	HPY101291	62%	100%	100%
SAU802240	KPN305016	69%	66.4%	98.8%
SAU802240	LMO100716	92%	100%	100%
SAU802240	MCA100153	67%	100%	100%
SAU802240	MAV102065	75%	100%	100%
SAU802240	MBV101638	75%	100%	100%
SAU802240	MLP101127	73%	92.6%	100%
SAU802240	MTU200711	75%	100%	100%
SAU802240	MGE100164	60%	100%	100%
SAU802240	MPN100656	61%	100%	100%
SAU802240	NGO100934	65%	100%	100%
SAU802240	NME200113	65%	100%	100%
SAU802240	PMU101405	69%	100%	100%
SAU802240	PRT103251	65%	97.5%	100%
SAU802240	PAE204251	66%	100%	100%
SAU802240	PPU108200	65%	100%	100%
SAU802240	PSY100106	65%	100%	100%
SAU802240	SPA104303	67%	100%	100%
SAU802240	STY101805	67%	100%	100%
SAU802240	SAU802240	100%	100%	100%
SAU802240	SEP200262	97%	100%	100%
SAU802240	SHA100778	99%	100%	85.3%
SAU802240	SMU100606	90%	100%	100%
SAU802240	SPN400199	89%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802240	SPY200047	88%	100%	100%
SAU802240	TPA100197	63%	100%	100%
SAU802240	UUR100243	63%	100%	100%
SAU802240	VCH102549	66%	100%	100%
SAU802240	YPS002449	68%	100%	100%
SAU802241	BAN105005	88%	100%	100%
SAU802241	BFR100428	53%	96.6%	98.8%
SAU802241	BPT104067	49%	93.1%	87.1%
SAU802241	BBU100486	51%	92.0%	95.2%
SAU802241	BCE100913	51%	93.1%	90%
SAU802241	BFU103897	61%	39.1%	75.6%
SAU802241	BMA102592	54%	93.1%	90%
SAU802241	CJU101602	45%	85.1%	89.2%
SAU802241	CPN200107	53%	89.7%	89.5%
SAU802241	CTR200795	52%	89.7%	92.8%
SAU802241	CAC101333	62%	94.3%	97.6%
SAU802241	CBO101908	57%	94.3%	97.6%
SAU802241	CDF102812	64%	93.1%	96.4%
SAU802241	CDP102662	54%	94.3%	89.1%
SAU802241	EBC103647	49%	86.2%	89.3%
SAU802241	EFA205257	80%	97.7%	89.5%
SAU802241	EFM201704	77%	96.6%	95.5%
SAU802241	ECO103234	49%	86.2%	89.3%
SAU802241	HIN100766	53%	86.2%	88.2%
SAU802241	HPY101292	46%	86.2%	87.2%
SAU802241	KPN204999	49%	86.2%	89.3%
SAU802241	LMO101712	77%	100%	100%
SAU802241	MCA101811	55%	90.8%	87.8%
SAU802241	MAV102052	55%	93.1%	69.2%
SAU802241	MBV101010	55%	93.1%	59.6%
SAU802241	MLP101128	56%	93.1%	63.8%
SAU802241	MTU200707	55%	93.1%	59.6%
SAU802241	MGE100163	50%	94.3%	97.6%
SAU802241	MPN100657	55%	94.3%	97.6%
SAU802241	NGO102122	53%	96.6%	96.6%
SAU802241	NME200114	53%	96.6%	96.6%
SAU802241	PMU101406	56%	86.2%	88.2%
SAU802241	PRT103498	42%	78.2%	100%
SAU802241	PAE204252	53%	89.7%	88.6%
SAU802241	PPU104520	55%	89.7%	86.7%
SAU802241	PSY107655	52%	89.7%	88.6%
SAU802241	SPA104305	36%	83.9%	86.9%
SAU802241	STY101804	49%	86.2%	89.3%
SAU802241	SAU802241	100%	100%	100%
SAU802241	SEP200263	96%	100%	100%
SAU802241	SHA100777	97%	100%	100%
SAU802241	SMU100607	74%	97.7%	98.8%
SAU802241	SPN400198	77%	97.7%	98.8%
SAU802241	SPY200046	74%	97.7%	98.8%
SAU802241	TPA100196	56%	94.3%	97.6%
SAU802241	UUR100242	54%	94.3%	97.6%
SAU802241	VCH102550	50%	88.5%	91.7%
SAU802241	YPS002447	45%	86.2%	89.3%
SAU802243	ABA100087	52%	81.2%	98.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802243	BAN105442	79%	100%	100%
SAU802243	BFR12478	57%	94.4%	94.4%
SAU802243	BPT104060	55%	93.1%	97.1%
SAU802243	BBU100484	59%	95.1%	99.3%
SAU802243	BCE110254	55%	93.8%	97.8%
SAU802243	BFU100274	55%	93.8%	97.8%
SAU802243	BMA108797	56%	93.8%	97.8%
SAU802243	CJU101604	62%	93.8%	95.7%
SAU802243	CPN200105	58%	94.4%	98.6%
SAU802243	CTR200797	59%	94.4%	98.6%
SAU802243	CAC102622	63%	99.3%	99.3%
SAU802243	CBO103643	66%	99.3%	99.3%
SAU802243	CDF100749	69%	97.2%	100%
SAU802243	CDP101572	63%	50.7%	97.3%
SAU802243	EBC103654	55%	93.1%	97.8%
SAU802243	EFA201987	74%	99.3%	99.3%
SAU802243	EFM200770	73%	99.3%	99.3%
SAU802243	ECO103236	54%	93.1%	97.8%
SAU802243	HIN100764	55%	93.1%	97.8%
SAU802243	HPY101294	55%	93.8%	95.7%
SAU802243	KPN300638	53%	86.8%	100%
SAU802243	LMO101423	74%	100%	100%
SAU802243	MCA100019	57%	93.1%	97.8%
SAU802243	MAV102093	55%	94.4%	98.6%
SAU802243	MBV101012	55%	94.4%	98.6%
SAU802243	MLP101130	56%	94.4%	98.6%
SAU802243	MTU200705	57%	94.4%	98.6%
SAU802243	MGE100161	55%	94.4%	98.6%
SAU802243	MPN100659	56%	95.1%	98.6%
SAU802243	NGO100936	56%	93.8%	97.8%
SAU802243	NME200116	56%	93.8%	97.8%
SAU802243	PMU101408	55%	93.1%	97.8%
SAU802243	PRT100078	55%	93.1%	97.8%
SAU802243	PAE204254	58%	93.1%	97.8%
SAU802243	PPU104518	57%	93.1%	97.8%
SAU802243	PSY103397	56%	93.1%	97.8%
SAU802243	SPA104307	54%	93.1%	97.8%
SAU802243	STY101803	54%	93.1%	97.8%
SAU802243	SAU802243	100%	100%	100%
SAU802243	SEP200265	97%	100%	100%
SAU802243	SHA100775	99%	100%	100%
SAU802243	SMU100608	75%	93.8%	98.5%
SAU802243	SPN400196	74%	93.8%	98.5%
SAU802243	SPY200044	74%	93.8%	98.5%
SAU802243	TPA100194	53%	92.4%	95.7%
SAU802243	UUR100240	57%	94.4%	98.6%
SAU802243	VCH102552	54%	93.8%	98.5%
SAU802243	YPS002443	58%	93.1%	97.8%
SAU802244	ABA100086	54%	95.4%	90.0%
SAU802244	BAN112122	74%	83.4%	100%
SAU802244	BAN102487	75%	100%	100%
SAU802244	BFR10672	54%	94.9%	84.4%
SAU802244	BPT100851	50%	95.4%	79.1%
SAU802244	BBU100483	47%	100%	75.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802244	BCE110191	51%	95.4%	78.2%
SAU802244	BFU100273	51%	95.4%	90.8%
SAU802244	BMA108753	51%	95.4%	78.2%
SAU802244	CJU101605	52%	95.4%	89.3%
SAU802244	CPN200104	50%	94.5%	92.4%
SAU802244	CTR200798	47%	98.6%	96.9%
SAU802244	CAC103109	64%	96.8%	95.5%
SAU802244	CBO100517	61%	96.8%	95.1%
SAU802244	CDF100748	58%	97.2%	78.6%
SAU802244	CDP101570	50%	98.2%	83.6%
SAU802244	EBC103657	55%	95.4%	89.3%
SAU802244	EFA201993	77%	100%	100%
SAU802244	EFM201332	76%	100%	100%
SAU802244	ECO103237	55%	95.4%	89.3%
SAU802244	HIN100763	58%	95.4%	88.5%
SAU802244	HPY101295	54%	95.4%	88.9%
SAU802244	KPN300639	55%	95.4%	89.7%
SAU802244	LMO101810	77%	100%	100%
SAU802244	MCA100254	52%	98.2%	89.2%
SAU802244	MAV102092	50%	96.8%	75.4%
SAU802244	MBV101013	50%	96.8%	77.0%
SAU802244	MLP101131	50%	96.8%	75.1%
SAU802244	MTU200704	50%	96.8%	77.0%
SAU802244	MGE100160	42%	94.9%	78.4%
SAU802244	MPN100660	41%	94.9%	76.9%
SAU802244	NGO100939	52%	93.1%	88.3%
SAU802244	NME200117	53%	93.1%	88.3%
SAU802244	PMU101409	58%	95.4%	88.5%
SAU802244	PRT103066	55%	95.4%	89.3%
SAU802244	PAE204255	57%	95.4%	91.2%
SAU802244	PPU104517	56%	95.4%	87.8%
SAU802244	PSY103396	56%	95.4%	91.2%
SAU802244	SPA104309	55%	95.4%	89.3%
SAU802244	STY101802	55%	95.4%	89.3%
SAU802244	SAU802244	100%	100%	100%
SAU802244	SEP200267	96%	100%	100%
SAU802244	SHA100774	97%	100%	100%
SAU802244	SMU100609	72%	100%	100%
SAU802244	SPN400195	74%	100%	100%
SAU802244	SPY200043	74%	100%	100%
SAU802244	TPA100193	53%	94.0%	83.8%
SAU802244	UUR100239	47%	96.8%	83.3%
SAU802244	VCH102553	55%	95.4%	89.3%
SAU802244	YPS002439	56%	95.4%	89.7%
SAU802245	ABA100085	50%	91.5%	97.3%
SAU802245	BAN109858	63%	95.7%	99.1%
SAU802245	BAN111310	73%	95.7%	99.1%
SAU802245	BFR102815	40%	88.0%	89.0%
SAU802245	BPT104052	43%	91.5%	98.2%
SAU802245	BBU100482	34%	92.3%	90.8%
SAU802245	BCE103775	43%	93.2%	100%
SAU802245	BFU100272	42%	93.2%	100%
SAU802245	BMA104499	43%	93.2%	100%
SAU802245	CJU101606	36%	97.4%	78.0%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802245	CPN200103	39%	90.6%	95.5%
SAU802245	CTR200799	38%	90.6%	95.5%
SAU802245	CAC102305	59%	93.2%	98.2%
SAU802245	CBO100872	53%	93.2%	98.2%
SAU802245	CDF103249	54%	94.9%	93.3%
SAU802245	CDP102437	57%	96.6%	94.2%
SAU802245	EBC103660	54%	93.2%	99.1%
SAU802245	EFA201995	66%	91.5%	91.5%
SAU802245	EFM202159	67%	91.5%	93.0%
SAU802245	ECO103238	54%	93.2%	99.1%
SAU802245	HIN100762	54%	93.2%	99.1%
SAU802245	HPY101296	40%	94.0%	86.9%
SAU802245	KPN300640	60%	36.8%	87.8%
SAU802245	LMO100543	74%	94.0%	93.2%
SAU802245	MCA100253	48%	93.2%	100%
SAU802245	MAV102091	53%	89.7%	58.3%
SAU802245	MBV101014	51%	89.7%	53.3%
SAU802245	MLP101132	52%	89.7%	60%
SAU802245	MTU200703	51%	89.7%	53.3%
SAU802245	MGE100159	41%	98.3%	79.9%
SAU802245	MPN100661	46%	91.5%	58.2%
SAU802245	NGO102695	46%	93.2%	100%
SAU802245	NME200118	46%	93.2%	100%
SAU802245	PMU101410	54%	93.2%	99.1%
SAU802245	PRT103067	53%	93.2%	99.1%
SAU802245	PAE204256	47%	93.2%	99.1%
SAU802245	PPU104507	47%	93.2%	99.1%
SAU802245	PSY107686	48%	77.8%	98.9%
SAU802245	SPA104311	54%	93.2%	99.1%
SAU802245	STY101801	54%	93.2%	99.1%
SAU802245	SAU802245	100%	100%	100%
SAU802245	SEP200269	99%	100%	100%
SAU802245	SHA100773	99%	100%	100%
SAU802245	SMU100610	63%	91.5%	93.9%
SAU802245	SPN400194	62%	91.5%	93.9%
SAU802245	SPY200042	65%	91.5%	93.9%
SAU802245	TPA100192	32%	90.6%	86.3%
SAU802245	UUR100238	44%	99.1%	37.6%
SAU802245	VCH102554	50%	93.2%	99.1%
SAU802245	YPS001865	53%	93.2%	99.1%
SAU802246	ABA100084	64%	98.9%	100%
SAU802246	BAN101977	68%	95.7%	96.6%
SAU802246	BAN110916	82%	100%	100%
SAU802246	BFR104321	64%	96.7%	100%
SAU802246	BPT104048	68%	98.9%	100%
SAU802246	BBU100481	58%	100%	100%
SAU802246	BCE112635	72%	95.7%	96.7%
SAU802246	BFU104367	72%	95.7%	96.7%
SAU802246	BMA100281	72%	95.7%	96.7%
SAU802246	CJU101607	61%	96.7%	95.7%
SAU802246	CPN200102	65%	90.2%	94.3%
SAU802246	CTR200800	65%	90.2%	94.3%
SAU802246	CAC101096	65%	97.8%	96.8%
SAU802246	CBO102193	60%	98.9%	86.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802246	CDF103424	67%	100%	98.9%
SAU802246	CDP101567	77%	100%	100%
SAU802246	EBC103663	65%	100%	100%
SAU802246	EFA201997	83%	100%	100%
SAU802246	EFM202484	82%	100%	100%
SAU802246	ECO103239	65%	100%	100%
SAU802246	HIN100761	65%	95.7%	96.7%
SAU802246	HPY101297	63%	96.7%	95.7%
SAU802246	KPN300699	64%	100%	100%
SAU802246	LMO100277	82%	100%	100%
SAU802246	MCA100252	59%	98.9%	100%
SAU802246	MAV102090	78%	100%	98.9%
SAU802246	MBV101015	78%	100%	98.9%
SAU802246	MLP101133	77%	100%	98.9%
SAU802246	MTU200702	78%	100%	98.9%
SAU802246	MGE100158	63%	93.5%	98.9%
SAU802246	MPN100662	66%	93.5%	98.9%
SAU802246	NGO102970	65%	100%	100%
SAU802246	NME200119	65%	100%	100%
SAU802246	PMU101411	65%	95.7%	96.7%
SAU802246	PRT100323	66%	100%	100%
SAU802246	PAE204257	62%	98.9%	100%
SAU802246	PPU111002	62%	98.9%	100%
SAU802246	PSY101086	61%	98.9%	100%
SAU802246	SPA104313	64%	100%	100%
SAU802246	STY101800	64%	100%	100%
SAU802246	SAU802246	100%	100%	100%
SAU802246	SEP200271	96%	100%	100%
SAU802246	SHA100772	96%	100%	100%
SAU802246	SMU102869	86%	41.3%	95%
SAU802246	SPN400192	85%	100%	98.9%
SAU802246	SPY200041	85%	100%	100%
SAU802246	TPA100191	52%	100%	100%
SAU802246	UUR100237	65%	90.2%	94.3%
SAU802246	VCH102555	63%	100%	100%
SAU802246	YPS001864	65%	100%	100%
SAU802247	ABA100083	54%	100%	100%
SAU802247	BAN100305	80%	58.1%	98.8%
SAU802247	BFR10675	60%	99.6%	100%
SAU802247	BPT100850	57%	99.6%	100%
SAU802247	BBU100480	57%	99.6%	100%
SAU802247	BCE100228	57%	99.6%	100%
SAU802247	BFU100271	59%	99.6%	100%
SAU802247	BMA102202	60%	99.6%	100%
SAU802247	CJU101608	59%	100%	100%
SAU802247	CPN200101	52%	98.6%	99.3%
SAU802247	CTR200801	51%	98.6%	99.3%
SAU802247	CAC101509	66%	100%	100%
SAU802247	CBO101184	68%	100%	100%
SAU802247	CDF100747	66%	99.6%	100%
SAU802247	CDP101565	63%	99.3%	97.5%
SAU802247	EBC103628	58%	99.6%	100%
SAU802247	EFA201999	78%	99.6%	100%
SAU802247	EFM200310	76%	83.0%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802247	ECO103240	58%	99.6%	100%
SAU802247	HIN100760	60%	99.6%	100%
SAU802247	HPY101298	57%	100%	100%
SAU802247	KPN300698	58%	99.6%	100%
SAU802247	LMO100597	84%	100%	100%
SAU802247	MCA100251	58%	100%	100%
SAU802247	MAV102089	62%	99.3%	97.5%
SAU802247	MBV101016	62%	99.3%	97.5%
SAU802247	MLP101134	60%	99.3%	97.5%
SAU802247	MTU200701	62%	99.3%	97.5%
SAU802247	MGE100157	60%	99.3%	98.6%
SAU802247	MPN100663	57%	99.3%	98.6%
SAU802247	NGO101613	62%	98.9%	98.2%
SAU802247	NME200120	62%	98.9%	98.2%
SAU802247	PMU101412	61%	99.6%	100%
SAU802247	PRT100324	60%	99.6%	100%
SAU802247	PAE204258	60%	99.3%	100%
SAU802247	PPU104505	59%	99.3%	100%
SAU802247	PSY107059	61%	99.3%	100%
SAU802247	SPA104315	57%	99.6%	100%
SAU802247	STY101789	57%	99.6%	100%
SAU802247	SAU802247	100%	100%	100%
SAU802247	SEP200273	95%	100%	100%
SAU802247	SHA100771	96%	100%	100%
SAU802247	SPN400191	76%	100%	100%
SAU802247	SPY200040	78%	100%	100%
SAU802247	TPA100190	57%	99.3%	100%
SAU802247	UUR100236	63%	99.3%	100%
SAU802247	VCH102556	61%	99.6%	100%
SAU802247	YPS001863	60%	100%	100%
SAU802248	ABA100082	40%	87.9%	76.4%
SAU802248	BFR102748	38%	94.5%	95.8%
SAU802248	BPT104043	39%	87.9%	82.7%
SAU802248	BBU100479	38%	98.9%	95.1%
SAU802248	BCE100645	41%	87.9%	77.9%
SAU802248	BFU103900	41%	87.9%	77.9%
SAU802248	BMA108040	41%	87.9%	77.9%
SAU802248	CJU101609	29%	86.8%	84.9%
SAU802248	CPN200100	34%	89.0%	91.9%
SAU802248	CTR200802	32%	89.0%	91.9%
SAU802248	CAC102428	51%	92.3%	85.7%
SAU802248	CBO102507	48%	90.1%	84.5%
SAU802248	CDF101975	49%	93.4%	88.5%
SAU802248	CDP102947	45%	97.8%	90.1%
SAU802248	EBC101608	37%	87.9%	81.8%
SAU802248	EFA205285	68%	97.8%	92.7%
SAU802248	ECO103241	38%	87.9%	81%
SAU802248	HIN100759	37%	87.9%	81.8%
SAU802248	KPN300697	38%	87.9%	81%
SAU802248	LMO100631	68%	97.8%	94.7%
SAU802248	MCA100250	43%	89.0%	76.1%
SAU802248	MAV102088	49%	97.8%	91%
SAU802248	MBV101017	50%	97.8%	91%
SAU802248	MLP101135	50%	97.8%	91%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802248	MTU200700	50%	97.8%	91%
SAU802248	MGE100156	38%	93.4%	83.0%
SAU802248	MPN100664	34%	93.4%	37.1%
SAU802248	NGO102702	42%	83.5%	74.0%
SAU802248	NME200121	38%	87.9%	76.4%
SAU802248	PMU101413	39%	87.9%	81%
SAU802248	PRT100325	39%	87.9%	81%
SAU802248	PAE204259	38%	87.9%	81.8%
SAU802248	PPU102891	41%	87.9%	81.8%
SAU802248	PSY107072	35%	87.9%	81.8%
SAU802248	SPA104317	38%	87.9%	81%
SAU802248	STY101788	38%	87.9%	81%
SAU802248	SAU802248	100%	100%	100%
SAU802248	SEP200275	92%	100%	100%
SAU802248	SHA100770	93%	100%	100%
SAU802248	SPN400190	53%	98.9%	94.9%
SAU802248	SPY200039	56%	98.9%	94.9%
SAU802248	TPA100189	40%	93.4%	90.4%
SAU802248	UUR100235	30%	93.4%	84.8%
SAU802248	VCH102557	40%	87.9%	81%
SAU802248	YPS005095	38%	87.9%	81%
SAU802249	ABA100081	42%	94.7%	98%
SAU802249	BFR10676	45%	97.6%	98.1%
SAU802249	BPT100849	37%	95.7%	96.6%
SAU802249	BBU100478	40%	96.1%	96.2%
SAU802249	BCE103118	36%	97.1%	97.6%
SAU802249	BFU100270	36%	97.1%	97.6%
SAU802249	BMA104332	40%	62.3%	97.0%
SAU802249	CJU101610	35%	91.8%	92.2%
SAU802249	CPN200099	37%	94.7%	92.9%
SAU802249	CTR200803	40%	94.7%	92.8%
SAU802249	CAC100377	48%	99.0%	99.0%
SAU802249	CBO103307	47%	99.0%	99.0%
SAU802249	CDF100746	54%	99.0%	94.5%
SAU802249	CDP101562	43%	93.7%	89.9%
SAU802249	EBC101609	41%	90.8%	93.0%
SAU802249	EFA202001	61%	99.5%	99.5%
SAU802249	ECO103242	40%	92.3%	94.5%
SAU802249	HIN100758	38%	96.6%	99.5%
SAU802249	HPY101300	38%	91.8%	91.2%
SAU802249	KPN300696	39%	92.3%	94.5%
SAU802249	LMO102640	60%	99.5%	99.5%
SAU802249	MCA100249	40%	96.6%	99.5%
SAU802249	MAV102087	45%	93.7%	92.2%
SAU802249	MBV101018	43%	93.7%	87.4%
SAU802249	MLP101136	46%	93.7%	84.8%
SAU802249	MTU200699	43%	93.7%	87.4%
SAU802249	MGE100155	38%	99.5%	99.5%
SAU802249	MPN100665	37%	98.1%	98.1%
SAU802249	NGO101615	37%	96.1%	96.6%
SAU802249	NME200122	36%	96.1%	96.6%
SAU802249	PMU101414	39%	96.6%	99.5%
SAU802249	PRT103342	41%	92.8%	95.0%
SAU802249	PAE204260	46%	97.1%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802249	PPU104504	43%	97.1%	100%
SAU802249	PSY108736	43%	97.1%	100%
SAU802249	SPA104319	40%	92.3%	95%
SAU802249	STY101787	40%	92.3%	94.5%
SAU802249	SAU802249	100%	100%	100%
SAU802249	SEP200280	90%	99.5%	99.5%
SAU802249	SHA100769	89%	100%	100%
SAU802249	SMU101861	48%	15.0%	100%
SAU802249	SPN400189	63%	99.5%	99.5%
SAU802249	SPY200038	61%	99.5%	99.5%
SAU802249	TPA100188	38%	96.1%	92.1%
SAU802249	UUR100234	36%	98.6%	100%
SAU802249	VCH102558	44%	93.2%	96%
SAU802249	YPS001862	40%	92.8%	95.0%
SAU802250	ABA100080	50%	43.2%	98.0%
SAU802250	BFR10677	49%	94.5%	98.0%
SAU802250	BPT100848	46%	96.8%	91.3%
SAU802250	BBU100477	48%	96.8%	99.0%
SAU802250	BCE112456	45%	100%	99.5%
SAU802250	BFU100269	45%	98.2%	96.3%
SAU802250	BMA106660	45%	98.2%	96.3%
SAU802250	CJU101611	34%	92.7%	95.3%
SAU802250	CPN200098	41%	95.5%	95.9%
SAU802250	CTR200804	44%	95.5%	95.0%
SAU802250	CAC103369	55%	98.2%	99.5%
SAU802250	CBO101061	56%	98.2%	96.3%
SAU802250	CDF100745	57%	97.3%	98.1%
SAU802250	CDP100915	48%	98.2%	95.9%
SAU802250	EBC101610	42%	96.8%	98.6%
SAU802250	EFA202003	64%	98.2%	99.0%
SAU802250	ECO103243	43%	96.8%	98.6%
SAU802250	HIN100757	45%	96.8%	98.6%
SAU802250	HPY101301	33%	90%	92.7%
SAU802250	KPN300695	41%	40.9%	98.9%
SAU802250	LMO102018	66%	98.2%	99.0%
SAU802250	MCA100248	45%	98.2%	99.5%
SAU802250	MAV102086	49%	99.1%	98.6%
SAU802250	MBV100990	48%	99.1%	98.6%
SAU802250	MLP101137	49%	99.1%	98.2%
SAU802250	MTU200698	48%	99.1%	98.6%
SAU802250	MGE100154	39%	99.1%	82.9%
SAU802250	MPN100666	41%	97.7%	73.2%
SAU802250	NGO101617	46%	99.1%	99.5%
SAU802250	NME200123	46%	99.1%	99.5%
SAU802250	PMU101415	46%	96.8%	98.6%
SAU802250	PRT102977	45%	96.8%	98.6%
SAU802250	PAE204261	46%	98.2%	98.6%
SAU802250	PPU111511	45%	98.2%	98.6%
SAU802250	PSY106254	46%	98.2%	93.7%
SAU802250	SPA104320	43%	90.9%	92.3%
SAU802250	STY101786	45%	90.9%	92.3%
SAU802250	SAU802250	100%	100%	100%
SAU802250	SEP200281	91%	100%	100%
SAU802250	SHA100768	90%	59.5%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802250	SMU100611	65%	98.2%	98.6%
SAU802250	SPN400188	65%	99.1%	99.5%
SAU802250	SPY200037	64%	98.2%	98.6%
SAU802250	TPA100187	43%	97.3%	98.1%
SAU802250	UUR100233	44%	98.6%	90.1%
SAU802250	VCH102559	48%	96.8%	98.6%
SAU802250	YPS001861	43%	96.8%	98.6%
SAU802251	ABA100720	56%	64.7%	100%
SAU802251	BAN112470	86%	82.4%	100%
SAU802251	BFR102501	63%	97.1%	98.0%
SAU802251	BPT104019	64%	100%	85.7%
SAU802251	BBU100476	54%	99.0%	98.1%
SAU802251	BCE114850	65%	100%	82.3%
SAU802251	BFU100268	65%	100%	71.3%
SAU802251	BMA104676	65%	100%	99.0%
SAU802251	CJU101612	53%	96.1%	95.1%
SAU802251	CPN200200	65%	97.1%	94.3%
SAU802251	CTR200710	66%	97.1%	94.3%
SAU802251	CAC101769	78%	100%	100%
SAU802251	CBO101448	76%	100%	100%
SAU802251	CDF104153	80%	61.8%	100%
SAU802251	CDP100914	71%	99.0%	100%
SAU802251	EBC101611	64%	100%	99.0%
SAU802251	EFA205288	86%	100%	100%
SAU802251	ECO103244	62%	100%	99.0%
SAU802251	HIN100756	64%	100%	86.4%
SAU802251	HPY101302	58%	95.1%	93.3%
SAU802251	KPN304660	64%	100%	94.4%
SAU802251	LMO100137	88%	100%	100%
SAU802251	MCA101858	61%	100%	99.0%
SAU802251	MAV102085	71%	99.0%	100%
SAU802251	MBV100992	71%	99.0%	100%
SAU802251	MLP101138	71%	99.0%	100%
SAU802251	MTU200697	71%	99.0%	100%
SAU802251	MGE100153	43%	92.2%	88.7%
SAU802251	MPN100667	42%	92.2%	87.0%
SAU802251	NGO102546	65%	100%	99.0%
SAU802251	NME200127	65%	100%	99.0%
SAU802251	PMU101416	64%	100%	99.0%
SAU802251	PRT100142	64%	100%	99.0%
SAU802251	PAE204262	62%	100%	99.0%
SAU802251	PPU104502	61%	91.2%	98.9%
SAU802251	PSY106273	62%	100%	82.3%
SAU802251	SPA104323	54%	100%	94.6%
SAU802251	STY101785	64%	100%	99.0%
SAU802251	SAU802251	100%	100%	100%
SAU802251	SEP200282	99%	100%	100%
SAU802251	SHA102423	96%	100%	100%
SAU802251	SMU100612	75%	100%	100%
SAU802251	SPN400187	77%	100%	100%
SAU802251	SPY200036	76%	100%	100%
SAU802251	TPA100186	51%	99.0%	99.0%
SAU802251	UUR100232	51%	97.1%	98.0%
SAU802251	VCH102560	62%	100%	99.0%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802251	YPS005092	64%	100%	99.0%
SAU802254	BAN106323	36%	98.5%	100%
SAU802254	BAN107719	48%	99.6%	99.3%
SAU802254	BFR11341	34%	83.5%	87.4%
SAU802254	BPT100056	35%	84.8%	72.3%
SAU802254	BCE103151	34%	84.8%	90.6%
SAU802254	BFU100507	34%	84.8%	70.8%
SAU802254	BMA106704	35%	76.9%	91.9%
SAU802254	CAC102331	44%	99.6%	98.6%
SAU802254	CBO102358	46%	99.2%	98.5%
SAU802254	CDF103201	48%	99.6%	99.3%
SAU802254	EBC101583	28%	48.0%	82.8%
SAU802254	EFA201812	40%	97.6%	97.1%
SAU802254	EFM200904	35%	41.6%	100%
SAU802254	ECO101731	29%	80.0%	90.8%
SAU802254	HIN100424	31%	81.2%	93.7%
SAU802254	KPN302957	29%	80.0%	91.5%
SAU802254	LMO102705	47%	99.9%	99.4%
SAU802254	PMU100207	31%	81.2%	94.6%
SAU802254	PRT106061	29%	81.7%	92.4%
SAU802254	PPU110370	29%	68.2%	89.2%
SAU802254	PSY104995	30%	74.0%	88.2%
SAU802254	SPA100636	33%	24.6%	72.4%
SAU802254	STY102434	30%	87.6%	96.7%
SAU802254	STM103402	29%	80.0%	91.4%
SAU802254	SAU802254	100%	100%	100%
SAU802254	SEP200287	72%	100%	100%
SAU802254	SHA100701	73%	99.9%	99.6%
SAU802254	VCH102013	32%	79.0%	91.3%
SAU802254	YPS000729	29%	82.4%	95.0%
SAU802261	ABA100532	26%	98.2%	97.7%
SAU802261	BAN104054	25%	96.0%	98.2%
SAU802261	BAN111342	33%	99.7%	98.7%
SAU802261	BAN113400	37%	99.1%	49.8%
SAU802261	BAN109301	45%	99.8%	100%
SAU802261	BFR11719	25%	49.6%	97.6%
SAU802261	BPT102713	23%	97.4%	96.4%
SAU802261	BBU100139	26%	99.5%	48.9%
SAU802261	BCE101292	24%	97.1%	48.4%
SAU802261	BFU109876	23%	97.3%	50.7%
SAU802261	BFU100767	24%	97.1%	45.9%
SAU802261	BMA103699	23%	99.8%	97.6%
SAU802261	CJU100961	23%	51.4%	99.9%
SAU802261	CAC102232	36%	55.5%	9.3%
SAU802261	CDF100351	30%	29.3%	100%
SAU802261	CDF103505	27%	98.6%	95.9%
SAU802261	EBC101480	24%	97.5%	97.9%
SAU802261	EFA103690	20%	31.3%	93.3%
SAU802261	EFM200039	20%	31.3%	93.3%
SAU802261	ECO102034	24%	98.6%	97.0%
SAU802261	HIN100875	24%	98.2%	97.0%
SAU802261	HPY100600	23%	98.3%	97.9%
SAU802261	KPN304473	24%	98.7%	97.6%
SAU802261	LPN100210	22%	99.1%	97.0%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802261	LPN100247	22%	98.8%	98.4%
SAU802261	MCA102709	23%	98.6%	98.7%
SAU802261	NGO100607	22%	98.7%	97.1%
SAU802261	NME201818	23%	98.7%	97.1%
SAU802261	PMU101132	23%	97.6%	96.5%
SAU802261	PRT102325	24%	97.4%	95.7%
SAU802261	PAE202524	24%	98.3%	46.8%
SAU802261	PPU103094	25%	98.3%	98.8%
SAU802261	PSY102999	24%	98.9%	98.3%
SAU802261	SPA104062	22%	96.5%	97.5%
SAU802261	STY104173	24%	98.6%	97.0%
SAU802261	STM103910	23%	98.6%	97.0%
SAU802261	SAU802261	100%	100%	100%
SAU802261	SEP200295	75%	100%	99.7%
SAU802261	SHA100824	74%	99.1%	94.8%
SAU802261	VCH100898	23%	98.7%	97.1%
SAU802261	YPS003137	24%	50.4%	96.9%
SAU802262	BFR104711	26%	22.3%	25.9%
SAU802262	BBU100585	21%	93.6%	95.1%
SAU802262	CAC101449	29%	23.8%	32.4%
SAU802262	SAU802262	100%	100%	100%
SAU802262	SEP200301	80%	100%	100%
SAU802262	SHA100823	78%	100%	100%
SAU802262	SPN400540	26%	98.8%	98.3%
SAU802262	SPY200444	29%	91.9%	92.2%
SAU802273	ABA105779	30%	92.4%	94.2%
SAU802273	BAN100337	38%	97.6%	99.3%
SAU802273	BAN108929	48%	92.6%	98.5%
SAU802273	BAN104661	48%	98.8%	97.4%
SAU802273	BAN112052	50%	98.6%	95.9%
SAU802273	BAN113492	52%	97.4%	96.0%
SAU802273	BPT101119	31%	86.9%	89.5%
SAU802273	BCE114366	32%	90.2%	89.3%
SAU802273	BFU101148	33%	82.3%	83.0%
SAU802273	BMA103156	33%	83.8%	76.8%
SAU802273	CJU101433	28%	90.0%	93.2%
SAU802273	CAC103575	31%	88.3%	90.9%
SAU802273	CBO100240	28%	94.7%	97.8%
SAU802273	CDF101730	34%	90.2%	93.9%
SAU802273	CDP101687	29%	84.0%	86.8%
SAU802273	EBC102785	30%	94.7%	96.1%
SAU802273	EFA202358	31%	91.9%	95.8%
SAU802273	ECO100803	29%	90.0%	90.8%
SAU802273	HIN101417	33%	89.3%	91.8%
SAU802273	HPY100169	27%	87.4%	90.8%
SAU802273	KPN302747	31%	76.1%	76.4%
SAU802273	LMO100059	36%	97.6%	99.8%
SAU802273	MCA101689	35%	93.1%	94.1%
SAU802273	MAV101757	32%	90.7%	93.8%
SAU802273	MBV106113	32%	86.9%	93.6%
SAU802273	MLP100130	25%	94.3%	97.6%
SAU802273	MTU200437	31%	90.9%	94.8%
SAU802273	PMU100694	33%	94.7%	97.8%
SAU802273	PRT102031	28%	95.2%	95.9%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802273	PAE203911	30%	83.1%	84.3%
SAU802273	PAE203026	30%	90.5%	91.1%
SAU802273	PPU103226	30%	85.0%	86.0%
SAU802273	PSY102581	32%	78.8%	80.2%
SAU802273	SPA100308	26%	76.1%	89.3%
SAU802273	STY102410	30%	76.1%	76.0%
SAU802273	SAU802273	100%	100%	100%
SAU802273	SEP200335	74%	100%	100%
SAU802273	SHA101561	77%	100%	100%
SAU802273	VCH101503	31%	90.2%	61.6%
SAU802273	YPS002254	27%	95.2%	93.4%
SAU802275	BAN104975	53%	92.9%	91.7%
SAU802275	BPT101121	40%	86.3%	82.7%
SAU802275	BCE102933	33%	75%	63.9%
SAU802275	BFU100752	32%	75%	59.2%
SAU802275	BMA109380	35%	75%	62.6%
SAU802275	CJU100675	35%	83.9%	78.9%
SAU802275	CAC100345	36%	88.7%	89.1%
SAU802275	CBO103886	34%	85.1%	87.7%
SAU802275	CDF101203	41%	58.3%	58.7%
SAU802275	EBC102209	43%	87.5%	85.3%
SAU802275	EFA202344	32%	91.7%	93.1%
SAU802275	ECO100758	44%	87.5%	85.3%
SAU802275	HIN100319	32%	89.9%	77.2%
SAU802275	HPY100786	35%	84.5%	81.2%
SAU802275	KPN303581	43%	87.5%	85.3%
SAU802275	LMO101377	45%	92.9%	95.1%
SAU802275	MCA101697	47%	86.9%	76.2%
SAU802275	MAV104045	30%	92.3%	95%
SAU802275	MBV100621	30%	80.4%	73.5%
SAU802275	MLP100125	30%	91.7%	83.4%
SAU802275	MTU200973	30%	80.4%	73.5%
SAU802275	PMU102003	31%	85.7%	75.5%
SAU802275	PRT105678	31%	84.5%	73.3%
SAU802275	PAE203912	38%	86.3%	77.3%
SAU802275	PAE203027	44%	86.3%	79.9%
SAU802275	PPU101702	43%	86.3%	79.9%
SAU802275	PSY109125	43%	86.3%	79.9%
SAU802275	SPA102733	45%	87.5%	85.3%
SAU802275	STY102331	45%	87.5%	85.3%
SAU802275	STM102090	45%	87.5%	85.3%
SAU802275	SAU802275	100%	100%	100%
SAU802275	SEP200340	66%	98.8%	95.5%
SAU802275	SHA101559	73%	100%	98.2%
SAU802275	VCH101006	47%	86.3%	84.1%
SAU802275	YPS000774	28%	89.9%	77.9%
SAU802276	ABA105442	31%	65.6%	84.1%
SAU802276	BAN103191	31%	99.1%	99.4%
SAU802276	BAN103239	35%	98.8%	99.1%
SAU802276	BAN100839	43%	94.6%	95.0%
SAU802276	BAN102602	44%	94.6%	95.0%
SAU802276	BAN107456	42%	98.8%	99.1%
SAU802276	BAN112551	43%	99.1%	99.4%
SAU802276	BAN105516	43%	99.4%	99.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802276	BFR102200	32%	41.9%	61.3%
SAU802276	BPT100891	29%	71.6%	90.9%
SAU802276	BCE105273	28%	37.7%	72.9%
SAU802276	BFU102717	32%	60.8%	81.0%
SAU802276	BMA107045	32%	60.8%	81.0%
SAU802276	CDP101620	31%	65.6%	64.8%
SAU802276	EBC102784	31%	71.6%	96.7%
SAU802276	EFA202445	31%	45.5%	40.3%
SAU802276	ECO103890	33%	71.6%	96.7%
SAU802276	HIN101418	32%	60.5%	82.7%
SAU802276	HPY100801	32%	53.9%	69.4%
SAU802276	KPN302744	31%	71.6%	94.8%
SAU802276	LPN101229	33%	60.2%	53.6%
SAU802276	LMO101764	34%	98.8%	99.4%
SAU802276	MCA103599	32%	71.3%	90.2%
SAU802276	MCA100944	30%	71.6%	93.3%
SAU802276	MAV102617	29%	61.1%	52.3%
SAU802276	MBV102230	30%	72.8%	62.5%
SAU802276	MLP100495	29%	61.1%	52.7%
SAU802276	MTU203076	30%	72.8%	62.5%
SAU802276	NGO101068	31%	71.6%	93.4%
SAU802276	NME200347	31%	71.6%	93.4%
SAU802276	PMU100695	33%	60.5%	84.5%
SAU802276	PRT101552	39%	62.0%	82.7%
SAU802276	PAE204660	34%	60.8%	80.6%
SAU802276	PPU109704	36%	60.8%	80.9%
SAU802276	PSY102406	34%	60.8%	78.4%
SAU802276	SPA100132	29%	71.6%	95.6%
SAU802276	STY102652	32%	71.6%	94.0%
SAU802276	SAU802276	100%	100%	100%
SAU802276	SEP200343	68%	99.4%	99.7%
SAU802276	SHA101558	72%	100%	100%
SAU802276	SPN400608	32%	36.8%	37.7%
SAU802276	VCH103341	31%	71.3%	93.7%
SAU802276	YPS000463	29%	71.6%	94.0%
SAU802288	ABA104364	64%	100%	48.3%
SAU802288	BPT101328	64%	100%	100%
SAU802288	BCE114774	65%	99%	47.8%
SAU802288	BFU110403	65%	99%	81.8%
SAU802288	BMA101403	63%	99%	43.4%
SAU802288	EBC101014	62%	100%	38.3%
SAU802288	ECO201397	61%	100%	100%
SAU802288	ECO205623	61%	100%	100%
SAU802288	HIN100520	58%	99%	99%
SAU802288	KPN300384	60%	66%	80.5%
SAU802288	KPN307408	63%	100%	100%
SAU802288	MBV102038	62%	99%	99%
SAU802288	MTU201815	62%	99%	99%
SAU802288	PAE204860	66%	99%	99%
SAU802288	PPU110641	64%	99%	47.4%
SAU802288	PSY101839	61%	99%	99%
SAU802288	SAU802288	100%	100%	100%
SAU802288	SEP101087	92%	100%	48.3%
SAU802288	UUR100439	59%	99%	98.0%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802288	YPS001366	52%	99%	99%
SAU802290	ABA103748	60%	99.5%	99.8%
SAU802290	BPT101319	57%	99.5%	99.6%
SAU802290	BCE105583	60%	100%	100%
SAU802290	BFU110328	60%	100%	100%
SAU802290	BMA103367	60%	100%	100%
SAU802290	EBC100116	66%	50.8%	98.3%
SAU802290	EFM200086	28%	12.4%	13.9%
SAU802290	ECO205553	62%	100%	100%
SAU802290	ECO201399	62%	100%	100%
SAU802290	HIN100518	59%	100%	100%
SAU802290	HPY100070	57%	99.5%	99.6%
SAU802290	KPN304109	62%	99.3%	99.5%
SAU802290	LMO100028	36%	22.1%	19.5%
SAU802290	MBV102006	55%	99.5%	99.7%
SAU802290	MTU201817	55%	99.5%	99.7%
SAU802290	PRT105539	61%	99.3%	72.4%
SAU802290	PAE204863	59%	99.5%	99.8%
SAU802290	PPU110642	59%	99.3%	99.5%
SAU802290	PSY100871	60%	99.5%	99.8%
SAU802290	SAU802290	100%	100%	100%
SAU802290	SEP200371	90%	100%	70.4%
SAU802290	UUR100437	57%	99.6%	99.8%
SAU802290	YPS001373	54%	99.1%	99.3%
SAU802292	ABA102930	22%	97.4%	59.2%
SAU802292	BPT101315	21%	65.9%	76.3%
SAU802292	BCE112587	23%	96.5%	96.5%
SAU802292	BFU110332	23%	96.5%	96.5%
SAU802292	BMA109613	25%	96.5%	56.0%
SAU802292	EBC101190	21%	97.4%	96.9%
SAU802292	ECO201401	19%	97.4%	96.9%
SAU802292	ECO205579	19%	97.4%	96.9%
SAU802292	HIN100516	22%	80.8%	97.4%
SAU802292	HPY100067	26%	96.5%	86.6%
SAU802292	KPN304125	20%	97.4%	96.9%
SAU802292	MBV102008	24%	47.6%	49.3%
SAU802292	MTU201818	24%	47.6%	49.3%
SAU802292	PRT104531	25%	81.2%	89.3%
SAU802292	PAE204887	26%	95.6%	96.4%
SAU802292	PPU110665	20%	97.4%	96.9%
SAU802292	PSY100980	20%	96.5%	97.3%
SAU802292	STY101858	35%	24.5%	37.3%
SAU802292	SAU802292	100%	100%	100%
SAU802292	SEP200375	76%	100%	100%
SAU802292	UUR100435	40%	97.4%	90%
SAU802292	YPS001379	23%	96.5%	96.5%
SAU802293	ABA102567	60%	97.5%	97.5%
SAU802293	BPT100743	61%	97.5%	93.0%
SAU802293	BCE100299	62%	96.6%	91.6%
SAU802293	BFU110334	62%	97.1%	91.2%
SAU802293	BMA101911	61%	96.6%	91.2%
SAU802293	CJU100584	30%	78.9%	61.1%
SAU802293	CBO101376	28%	90.2%	78.0%
SAU802293	CDP100866	31%	92.2%	71.9%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802293	EBC101191	58%	94.1%	94.6%
SAU802293	ECO102667	27%	89.2%	59.3%
SAU802293	HIN100515	62%	99.5%	90.2%
SAU802293	HPY100066	61%	96.6%	99.0%
SAU802293	KPN304128	63%	97.1%	96.6%
SAU802293	LPN100384	30%	88.7%	67.9%
SAU802293	MBV102011	51%	98.0%	89.3%
SAU802293	MTU201819	51%	98.0%	89.3%
SAU802293	PRT102194	62%	93.6%	93.2%
SAU802293	PAE204888	58%	97.5%	97.5%
SAU802293	PPU110666	64%	93.6%	92.3%
SAU802293	PSY106880	57%	97.5%	97.1%
SAU802293	SPA101916	26%	89.2%	59.3%
SAU802293	STY102828	26%	89.2%	59.3%
SAU802293	STM103657	26%	89.2%	59.3%
SAU802293	SAU802293	100%	100%	100%
SAU802293	SEP200377	90%	100%	100%
SAU802293	UUR100434	71%	96.1%	95.6%
SAU802293	YPS001381	58%	95.1%	89.5%
SAU802308	BAN111346	23%	75.8%	96%
SAU802308	BAN104126	26%	68.8%	95.6%
SAU802308	BAN104809	28%	93.6%	92.5%
SAU802308	LMO101374	28%	96.2%	95.6%
SAU802308	SAU802308	100%	100%	100%
SAU802308	SHA101510	78%	100%	99.4%
SAU802309	ABA105410	27%	70.5%	78.5%
SAU802309	BAN111819	47%	98.6%	100%
SAU802309	BAN104504	48%	97.1%	98.0%
SAU802309	BAN108797	55%	98.6%	98.9%
SAU802309	BAN107861	56%	99.2%	99.5%
SAU802309	BFR102378	31%	7.2%	8.6%
SAU802309	BPT101897	29%	72.7%	94.8%
SAU802309	BCE100301	33%	86.3%	95.5%
SAU802309	BFU109099	33%	94.7%	91.4%
SAU802309	BMA102600	32%	99.1%	95.1%
SAU802309	CJU101426	27%	52.6%	58.4%
SAU802309	CAC102909	27%	20.4%	34.9%
SAU802309	CBO103110	26%	20.8%	36.6%
SAU802309	CDF102669	33%	53.9%	94.8%
SAU802309	EBC104465	34%	69.4%	96.4%
SAU802309	EFA202359	33%	95.2%	99.0%
SAU802309	ECO103973	35%	69.4%	96.2%
SAU802309	HIN101025	23%	49.8%	65.5%
SAU802309	HPY101249	22%	44.7%	46.1%
SAU802309	KPN300210	34%	8.1%	59.9%
SAU802309	KPN300277	25%	11.7%	93.5%
SAU802309	KPN300272	37%	14.4%	82.4%
SAU802309	KPN303260	32%	69.4%	96.2%
SAU802309	LPN103373	23%	76.1%	84.0%
SAU802309	LMO101763	54%	98.5%	97.1%
SAU802309	MCA101207	20%	83.2%	82.2%
SAU802309	MAV100466	29%	18.0%	93.3%
SAU802309	MAV103718	30%	20.1%	97.2%
SAU802309	MAV102918	30%	31.8%	32.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802309	MAV102797	32%	48.8%	97.0%
SAU802309	MBV102300	27%	34.2%	44.8%
SAU802309	MTU202862	27%	34.2%	44.8%
SAU802309	NGO100650	23%	75.2%	82.1%
SAU802309	NME200010	23%	75.2%	82.1%
SAU802309	PMU101594	28%	69.2%	95.3%
SAU802309	PRT106150	34%	69.1%	95.0%
SAU802309	PAE201778	30%	69.4%	77.3%
SAU802309	PPU106426	34%	94.2%	94.3%
SAU802309	PSY105562	29%	68.9%	76.8%
SAU802309	SPA101768	35%	69.1%	100%
SAU802309	STY102346	35%	69.4%	96.2%
SAU802309	STM101130	22%	63.4%	84.5%
SAU802309	SAU802309	100%	100%	100%
SAU802309	SHA101509	84%	90.5%	100%
SAU802309	VCH103400	28%	66.8%	91.9%
SAU802309	YPS003389	33%	69.5%	96.2%
SAU802310	BAN106020	40%	96.2%	99.7%
SAU802310	BAN100582	40%	96.8%	99.0%
SAU802310	CAC101564	31%	93.7%	90.0%
SAU802310	CAC101142	32%	94.9%	93.2%
SAU802310	CBO100290	30%	98.4%	72.9%
SAU802310	CDP100702	36%	55.6%	39.7%
SAU802310	EFA200704	36%	97.1%	99.0%
SAU802310	EFM200695	38%	98.1%	97.5%
SAU802310	LMO102536	33%	99.4%	97.8%
SAU802310	MAV105446	29%	69.5%	35.9%
SAU802310	MBV101890	26%	58.4%	33.5%
SAU802310	MLP100452	30%	60.6%	47.2%
SAU802310	MTU200816	26%	58.4%	33.5%
SAU802310	SAU802310	100%	100%	100%
SAU802310	SEP200407	76%	99.7%	99.4%
SAU802310	SHA101993	49%	98.1%	98.7%
SAU802310	SMU100754	29%	93.0%	74.9%
SAU802310	SPN401757	29%	94.0%	90.2%
SAU802310	SPY201332	30%	97.1%	75%
SAU802328	ABA103559	40%	91.1%	91.4%
SAU802328	BAN100208	35%	98.0%	97.9%
SAU802328	BAN105602	43%	98.3%	99.3%
SAU802328	BCE104059	55%	47.1%	75.8%
SAU802328	BCE105925	52%	86.3%	100%
SAU802328	BFU103430	45%	97.3%	98.6%
SAU802328	BMA102007	42%	92.5%	94.4%
SAU802328	CAC103127	44%	96.9%	93.0%
SAU802328	CBO102575	42%	93.2%	92.5%
SAU802328	EBC103168	57%	96.2%	97.6%
SAU802328	EFA200150	50%	99.0%	97.6%
SAU802328	EFM200978	49%	98.6%	97.3%
SAU802328	ECO102937	60%	97.6%	97.3%
SAU802328	KPN305078	55%	94.2%	90.2%
SAU802328	LMO101848	60%	100%	99.7%
SAU802328	MAV106410	45%	67.9%	97.5%
SAU802328	PAE202140	40%	96.6%	97.9%
SAU802328	PPU105455	45%	96.6%	98.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802328	PSY101078	46%	94.9%	96.5%
SAU802328	SPA103631	59%	97.3%	96.9%
SAU802328	STY100437	60%	97.3%	96.9%
SAU802328	STM101187	60%	97.3%	96.9%
SAU802328	SAU802328	100%	100%	100%
SAU802328	SEP200449	82%	100%	100%
SAU802328	SHA100524	84%	100%	100%
SAU802331	ABA105800	62%	98.6%	97.7%
SAU802331	BAN106204	54%	98.2%	98.9%
SAU802331	BAN105173	68%	98.4%	98.6%
SAU802331	BFR10261	34%	94.2%	81.8%
SAU802331	BCE104672	58%	58.2%	100%
SAU802331	BFU113421	61%	99.1%	97.5%
SAU802331	BMA109225	62%	99.1%	97.5%
SAU802331	EBC100807	58%	59.3%	100%
SAU802331	KPN301790	60%	98.4%	96.8%
SAU802331	LPN101472	60%	98.6%	98.2%
SAU802331	MCA101940	58%	98.7%	100%
SAU802331	PAE205095	62%	98.6%	97.5%
SAU802331	PPU106762	61%	98.6%	97.8%
SAU802331	PSY101331	62%	96.9%	94.4%
SAU802331	SPA101433	57%	98.2%	99.4%
SAU802331	STY102299	60%	98.4%	97.0%
SAU802331	STM101870	38%	9.9%	6.8%
SAU802331	SAU802331	100%	100%	100%
SAU802331	SPN400943	29%	11.6%	31.5%
SAU802331	SPY201590	36%	94.0%	79.9%
SAU802331	VCH101184	60%	98.9%	96.3%
SAU802331	YPS002693	60%	98.6%	96.8%
SAU802332	BPT100588	25%	97.6%	90.9%
SAU802332	BFU102473	22%	92.9%	91.4%
SAU802332	CBO102863	25%	97.3%	97.3%
SAU802332	EBC101843	25%	82.7%	82.5%
SAU802332	EFM102228	25%	78.6%	92.7%
SAU802332	ECO201939	26%	82.7%	82.3%
SAU802332	KPN307471	23%	94.9%	96.0%
SAU802332	MAV102104	23%	87.8%	81.9%
SAU802332	MBV105077	23%	79.3%	75.3%
SAU802332	MLP101570	23%	79.3%	76.8%
SAU802332	MTU200117	23%	79.3%	75.8%
SAU802332	PPU109373	29%	20.7%	20.5%
SAU802332	PPU101916	24%	92.5%	93.3%
SAU802332	PSY104413	24%	97.3%	94.2%
SAU802332	SPA103068	25%	80.6%	77.0%
SAU802332	STY104272	25%	80.6%	81.0%
SAU802332	STM101851	26%	81.0%	77.6%
SAU802332	SAU802332	100%	100%	100%
SAU802333	BAN111465	58%	98.6%	100%
SAU802333	BAN104289	58%	98.6%	100%
SAU802333	BAN108891	65%	99.3%	99.3%
SAU802333	BAN102504	64%	99.3%	100%
SAU802333	BCE105683	26%	78.4%	92.9%
SAU802333	BFU114968	32%	80.6%	20.6%
SAU802333	CBO102493	39%	51.1%	87.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802333	EBC103002	34%	96.4%	92.9%
SAU802333	EFA201396	28%	79.1%	93.5%
SAU802333	EFM201766	28%	81.3%	96.7%
SAU802333	ECO100187	29%	83.5%	89.9%
SAU802333	HIN100307	30%	79.9%	88.9%
SAU802333	KPN302981	35%	93.5%	92.1%
SAU802333	LPN101860	46%	23.0%	61.5%
SAU802333	LMO101925	35%	93.5%	100%
SAU802333	NGO101565	26%	78.4%	87.4%
SAU802333	NME201984	27%	78.4%	85.5%
SAU802333	PRT100522	28%	84.2%	96.9%
SAU802333	PAE201128	35%	94.2%	93.3%
SAU802333	PPU108454	24%	82.0%	83.2%
SAU802333	SPA101410	27%	79.1%	88.1%
SAU802333	STY100607	27%	79.1%	88.1%
SAU802333	SAU802333	100%	100%	100%
SAU802333	SEP202219	62%	98.6%	96.5%
SAU802333	SMU101103	25%	79.1%	90%
SAU802333	SPN400864	24%	83.5%	85.3%
SAU802333	YPS002942	27%	79.1%	88.1%
SAU802335	CBO103499	20%	58.0%	68.6%
SAU802335	CDF103594	24%	43.2%	87.3%
SAU802335	SAU802335	100%	100%	100%
SAU802335	SEP200455	58%	100%	99.5%
SAU802335	SHA103355	56%	100%	99.7%
SAU802341	ABA100592	34%	72.6%	18.3%
SAU802341	BAN106164	42%	18.1%	53.5%
SAU802341	BAN101097	46%	98.0%	99.3%
SAU802341	BFR10398	27%	92.0%	97.2%
SAU802341	BPT100190	32%	70.2%	61.0%
SAU802341	BCE110810	30%	75.6%	91.9%
SAU802341	BFU103371	31%	70.2%	84.7%
SAU802341	BMA108770	30%	75.6%	91.9%
SAU802341	CJU100624	32%	78.3%	98.8%
SAU802341	CAC101062	27%	98.7%	98.4%
SAU802341	CAC101497	28%	99.3%	99.0%
SAU802341	CBO100997	30%	98.0%	97.4%
SAU802341	CDF103190	30%	97.0%	97.7%
SAU802341	CDP101422	32%	77.6%	85.3%
SAU802341	EBC103391	27%	99.3%	97.7%
SAU802341	EFA202336	42%	99.0%	99.3%
SAU802341	EFM200486	41%	99.3%	99.7%
SAU802341	ECO100770	31%	97.3%	4.8%
SAU802341	HPY100705	32%	71.9%	91.7%
SAU802341	KPN303592	30%	97.3%	4.8%
SAU802341	LMO100853	48%	98.7%	98.7%
SAU802341	MCA101024	30%	75.6%	95.9%
SAU802341	MAV103194	30%	96.0%	89.8%
SAU802341	MBV100156	30%	96.0%	90.7%
SAU802341	MTU201201	30%	96.0%	90.7%
SAU802341	MPN100502	28%	76.9%	72.1%
SAU802341	NGO101385	34%	72.9%	70.8%
SAU802341	NME200704	36%	66.2%	91.7%
SAU802341	PMU100171	29%	77.6%	98.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802341	PRT103445	28%	75.6%	96.3%
SAU802341	PAE203670	31%	97.0%	97.4%
SAU802341	PAE204034	33%	71.6%	70.1%
SAU802341	PPU104145	29%	77.6%	98.8%
SAU802341	PSY100293	30%	77.6%	98.8%
SAU802341	SPA102971	29%	97.3%	5.0%
SAU802341	STM103062	26%	99.3%	97.7%
SAU802341	SAU802341	100%	100%	100%
SAU802341	SMU100271	35%	72.9%	75.2%
SAU802341	SPN401561	40%	96.3%	97.0%
SAU802341	SPY200545	29%	94.0%	93.2%
SAU802341	UUR100092	32%	70.2%	89.8%
SAU802341	VCH102491	32%	77.6%	98.8%
SAU802346	ABA104933	22%	51.6%	44.6%
SAU802346	BAN109344	42%	97.4%	100%
SAU802346	BAN107706	43%	97.4%	97.4%
SAU802346	BBU100683	27%	94.3%	92.8%
SAU802346	BCE111066	25%	23.5%	21.5%
SAU802346	BFU102030	29%	24.4%	20.5%
SAU802346	CBO101704	22%	88.3%	85.2%
SAU802346	CDF103639	24%	46.1%	41.8%
SAU802346	EBC103192	22%	49.3%	43.0%
SAU802346	EFA200385	46%	96.6%	97.4%
SAU802346	EFM202514	45%	96.8%	95.5%
SAU802346	ECO103527	24%	49.3%	41.2%
SAU802346	HIN101704	24%	42.7%	34.1%
SAU802346	KPN305761	21%	53.6%	45.2%
SAU802346	LPN100706	36%	36.7%	70.6%
SAU802346	LPN100340	32%	92.6%	97.4%
SAU802346	LMO101142	43%	98.6%	96.6%
SAU802346	MCA101122	26%	35.0%	26.1%
SAU802346	MAV101346	30%	86.5%	91.6%
SAU802346	MBV104099	24%	36.4%	28.0%
SAU802346	MTU200691	24%	36.4%	28.0%
SAU802346	NGO101059	25%	45.6%	35.6%
SAU802346	NME201451	25%	45.6%	35.6%
SAU802346	PMU100288	23%	31.8%	30.7%
SAU802346	PAE204767	22%	49.3%	42.8%
SAU802346	PPU108584	23%	49.3%	42.8%
SAU802346	STY100378	21%	49.3%	41.2%
SAU802346	STM104153	22%	49.3%	41.2%
SAU802346	SAU802346	100%	100%	100%
SAU802346	SEP200052	76%	99.7%	99.7%
SAU802346	SEP200853	76%	99.7%	99.7%
SAU802346	SHA102078	79%	100%	100%
SAU802346	SMU100940	40%	90.5%	94.0%
SAU802346	SPN400341	40%	90.5%	92.6%
SAU802346	SPY200654	42%	90.5%	94.5%
SAU802346	VCH103702	26%	33.8%	33.3%
SAU802346	YPS003024	24%	43.3%	34.6%
SAU802359	BAN112546	46%	98.2%	100%
SAU802359	BAN108719	49%	98.2%	97.8%
SAU802359	BMA108659	36%	99.5%	94.4%
SAU802359	CDP101457	42%	93.7%	91.0%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802359	LMO101705	48%	100%	100%
SAU802359	SAU802359	100%	100%	100%
SAU802359	SEP200905	70%	99.1%	98.6%
SAU802359	SHA101961	68%	99.1%	99.1%
SAU802360	BFR101675	24%	30.2%	27.9%
SAU802360	BFR101280	28%	31.3%	34.9%
SAU802360	BFR105907	25%	28.2%	25%
SAU802360	BMA100570	24%	33.6%	32.0%
SAU802360	CDF100955	21%	98.9%	44.4%
SAU802360	CDF102346	19%	100%	99.2%
SAU802360	ECO101089	20%	44.7%	41.4%
SAU802360	MTU202526	18%	98.6%	98.6%
SAU802360	SAU802360	100%	100%	100%
SAU802360	SEP200907	53%	100%	100%
SAU802360	SHA102644	56%	100%	100%
SAU802360	VCH103501	30%	33.3%	15.2%
SAU802365	BAN104884	56%	93.5%	96.2%
SAU802365	BAN101178	62%	95.7%	98%
SAU802365	BCE112448	51%	91.4%	89.5%
SAU802365	CJU100361	24%	84.1%	92.4%
SAU802365	CDP100511	49%	95.9%	98.4%
SAU802365	EBC106483	48%	95.7%	89.8%
SAU802365	ECO102168	50%	91.8%	86.1%
SAU802365	HPY100084	23%	84.1%	91.3%
SAU802365	KPN301561	47%	96.1%	90.8%
SAU802365	MAV102823	46%	94.7%	96.4%
SAU802365	MBV100580	46%	94.1%	99.4%
SAU802365	MTU202814	47%	95.1%	98.6%
SAU802365	NGO100920	49%	94.7%	99.2%
SAU802365	NME200310	50%	94.7%	99.2%
SAU802365	PRT100644	49%	94.5%	97.2%
SAU802365	PAE203450	53%	94.5%	93.1%
SAU802365	PPU104014	51%	94.1%	96.0%
SAU802365	PSY100602	49%	94.5%	96.4%
SAU802365	SAU802365	100%	100%	100%
SAU802365	SEP200913	79%	96.3%	100%
SAU802365	SHA101955	77%	96.3%	100%
SAU802365	VCH102882	31%	10.6%	12.9%
SAU802368	SAU802368	100%	100%	100%
SAU802368	SEP200934	44%	99.5%	99.5%
SAU802369	BAN103259	36%	97.7%	97.1%
SAU802369	BAN112183	36%	97.7%	97.1%
SAU802369	BPT100938	43%	26.9%	28.6%
SAU802369	BCE107689	29%	97.1%	95.0%
SAU802369	BFU103812	35%	37.4%	36.8%
SAU802369	BMA103339	24%	60.2%	60.6%
SAU802369	EBC105348	22%	89.5%	89.4%
SAU802369	EFA202072	42%	98.8%	99.4%
SAU802369	EFM200209	35%	97.7%	96.5%
SAU802369	KPN303262	31%	98.2%	97.7%
SAU802369	LMO102096	40%	98.2%	100%
SAU802369	MAV105704	28%	93.6%	89.0%
SAU802369	MBV105099	26%	93.6%	98.1%
SAU802369	MTU202632	26%	93.6%	98.1%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802369	NME200232	28%	43.3%	42.9%
SAU802369	PRT106021	25%	78.9%	79.1%
SAU802369	PPU108805	28%	48.0%	49.7%
SAU802369	PSY102532	24%	97.1%	94.3%
SAU802369	SPA102323	26%	67.8%	72.3%
SAU802369	STY103987	32%	46.8%	46.2%
SAU802369	SAU802369	100%	100%	100%
SAU802369	SEP202650	51%	97.7%	93.3%
SAU802369	SHA100368	52%	100%	100%
SAU802369	SMU100484	36%	97.7%	96.5%
SAU802369	SPN400508	36%	98.2%	99.4%
SAU802369	SPY101945	37%	93.0%	97.0%
SAU802369	VCH101321	34%	32.2%	34.8%
SAU802369	YPS000948	31%	46.8%	47.3%
SAU802371	BAN103862	34%	36.8%	32.2%
SAU802371	BFR102730	26%	59.4%	52.7%
SAU802371	BCE108880	26%	70.7%	61.2%
SAU802371	BFU115699	25%	65.4%	63.9%
SAU802371	CAC101368	28%	89.5%	86.4%
SAU802371	EBC104604	29%	39.8%	32.6%
SAU802371	KPN302220	43%	91.7%	86.3%
SAU802371	LMO101023	42%	94.7%	92.7%
SAU802371	PRT104530	29%	66.2%	28.2%
SAU802371	SAU802371	100%	100%	100%
SAU802371	SEP200943	68%	100%	100%
SAU802371	SHA101897	60%	100%	100%
SAU802371	SMU100213	38%	35.3%	26.1%
SAU802371	SPN400237	30%	49.6%	47.8%
SAU802372	BAN103594	38%	32.9%	85.8%
SAU802372	BAN100580	37%	63.1%	98.6%
SAU802372	BAN108168	43%	99.1%	94.0%
SAU802372	BFU101355	27%	91.8%	85.6%
SAU802372	EFA200225	31%	93.1%	90.2%
SAU802372	EFM200250	32%	91.5%	89.5%
SAU802372	LMO102184	33%	96.1%	94.3%
SAU802372	SAU802372	100%	100%	100%
SAU802372	SHA101896	68%	99.7%	96.2%
SAU802372	SMU100809	34%	91.8%	90.4%
SAU802372	SPN401420	32%	93.1%	92.9%
SAU802372	SPY200633	34%	91.8%	90.9%
SAU802378	PRT102873	30%	41.8%	29.1%
SAU802378	SAU802378	100%	100%	100%
SAU802378	SEP200955	54%	65.2%	82.4%
SAU802378	SHA100322	56%	65.2%	83.1%
SAU802378	SPY200567	35%	50.6%	65.6%
SAU802389	BAN103843	25%	58.9%	77.4%
SAU802389	BAN108506	23%	68.1%	74.8%
SAU802389	CDF101015	40%	98.4%	95%
SAU802389	SAU802389	100%	100%	100%
SAU802389	SEP100573	38%	15.1%	50%
SAU802389	SMU101334	42%	97.4%	97.7%
SAU802389	UUR100585	22%	79.6%	44.1%
SAU802390	ABA100515	30%	38.2%	92.2%
SAU802390	BAN111977	22%	93.5%	98.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802390	BAN110775	23%	93.5%	96.3%
SAU802390	BPT104469	25%	39.0%	71.5%
SAU802390	BCE109138	32%	37.0%	44.2%
SAU802390	BMA105986	34%	37.0%	63.9%
SAU802390	CAC101199	26%	93.5%	97.9%
SAU802390	CBO101857	24%	95.9%	98.8%
SAU802390	CDF102948	27%	58.5%	55.3%
SAU802390	CDF101305	33%	46.3%	41.6%
SAU802390	CDF102920	26%	93.1%	96.4%
SAU802390	CDP101417	21%	92.7%	94.1%
SAU802390	EBC101808	30%	40.7%	97.1%
SAU802390	EFA201158	26%	95.5%	98.4%
SAU802390	EFM202323	24%	93.1%	97.6%
SAU802390	KPN307759	31%	37.0%	93.9%
SAU802390	LMO101047	25%	94.7%	98.8%
SAU802390	MAV100400	29%	40.2%	33.1%
SAU802390	PRT100890	31%	38.6%	94.1%
SAU802390	PPU110548	26%	46.7%	89.8%
SAU802390	STM103457	28%	38.2%	90.9%
SAU802390	SAU802390	100%	100%	100%
SAU802390	SEP200173	33%	96.3%	98.8%
SAU802390	SHA101547	30%	94.7%	95.4%
SAU802390	SMU101335	41%	95.1%	98.4%
SAU802390	SPN400649	30%	47.6%	56.4%
SAU802390	VCH100958	24%	40.7%	77.0%
SAU802390	YPS003904	24%	52.0%	45.5%
SAU802397	BAN101011	45%	99.0%	99.3%
SAU802397	BAN102461	58%	99.6%	99.1%
SAU802397	BMA109820	49%	98.9%	92.5%
SAU802397	CDP101676	60%	26.0%	97.0%
SAU802397	EBC101930	47%	57.4%	98.3%
SAU802397	ECO101197	49%	99.3%	98.2%
SAU802397	KPN305068	48%	99.4%	98.3%
SAU802397	MCA101683	49%	99.5%	98.2%
SAU802397	MAV100250	49%	98.9%	95.3%
SAU802397	MBV101452	49%	98.9%	98.1%
SAU802397	MTU201146	49%	98.9%	98.1%
SAU802397	PRT105206	49%	97.9%	96.5%
SAU802397	PAE203872	49%	99.6%	97.9%
SAU802397	SPA102910	47%	52.2%	100%
SAU802397	STY102963	50%	98.7%	97.5%
SAU802397	STM100368	49%	98.0%	96.9%
SAU802397	SAU802397	100%	100%	100%
SAU802397	SEP202550	86%	100%	100%
SAU802397	SHA101605	86%	100%	100%
SAU802398	ABA103247	41%	73.5%	52.3%
SAU802398	BAN106629	40%	73.8%	75.5%
SAU802398	BAN112655	41%	73.8%	50.6%
SAU802398	BFR12474	22%	74.5%	39.6%
SAU802398	BPT100993	36%	73.5%	48.7%
SAU802398	BCE103181	34%	74.5%	98.8%
SAU802398	BFU106371	39%	71.1%	91.6%
SAU802398	BMA101721	38%	71.7%	83.1%
SAU802398	CAC103696	37%	73.8%	48.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802398	CBO100144	36%	73.5%	49.0%
SAU802398	CDF102901	38%	83.1%	54.4%
SAU802398	CDP100485	40%	64.9%	98.6%
SAU802398	EBC103863	36%	76.3%	53.6%
SAU802398	ECO103291	37%	76.3%	53.6%
SAU802398	KPN306621	38%	71.7%	49.0%
SAU802398	LMO101561	35%	85.5%	56.8%
SAU802398	MCA103517	38%	72.3%	52.3%
SAU802398	MAV102832	34%	72.3%	59.1%
SAU802398	MBV103227	34%	72%	58.3%
SAU802398	MTU202809	34%	72%	58.3%
SAU802398	NME201254	38%	77.8%	53.1%
SAU802398	PRT104849	36%	73.5%	51.3%
SAU802398	PAE202609	41%	71.7%	50.1%
SAU802398	PPU100873	41%	72.9%	51.2%
SAU802398	PSY104166	41%	73.8%	51.7%
SAU802398	SPA103180	35%	76.3%	53.6%
SAU802398	STY101423	35%	76.3%	53.6%
SAU802398	STM102832	36%	76.3%	53.6%
SAU802398	SAU802398	100%	100%	100%
SAU802398	SEP201014	60%	94.2%	97.7%
SAU802398	SHA101604	59%	96.3%	99.7%
SAU802398	SPY100086	33%	38.8%	40.9%
SAU802398	VCH102524	38%	71.7%	77.3%
SAU802398	YPS000102	37%	78.5%	53.6%
SAU802399	ABA103234	36%	80.8%	83.2%
SAU802399	BAN109784	56%	98.1%	82.9%
SAU802399	BAN101731	56%	98.1%	86.4%
SAU802399	BPT100852	27%	94.2%	95.1%
SAU802399	BCE102364	37%	60.6%	59.3%
SAU802399	BMA104059	41%	94.2%	63.6%
SAU802399	EBC103872	29%	92.3%	94.4%
SAU802399	ECO103289	31%	90.4%	92.6%
SAU802399	KPN303056	35%	75%	72.9%
SAU802399	LPN102471	32%	52.9%	47.0%
SAU802399	MAV106074	31%	90.4%	81.0%
SAU802399	MBV100699	68%	18.3%	6.2%
SAU802399	MTU203475	40%	42.3%	11.4%
SAU802399	PAE201779	36%	94.2%	90.7%
SAU802399	PSY107850	41%	30.8%	43.6%
SAU802399	SAU802399	100%	100%	100%
SAU802399	SEP201015	69%	100%	100%
SAU802399	SHA101603	76%	100%	100%
SAU802399	YPS000211	28%	92.3%	90.6%
SAU802400	ABA101297	35%	99.0%	94.9%
SAU802400	BAN105525	60%	21.7%	97.8%
SAU802400	BAN103462	47%	99.8%	100%
SAU802400	BAN107337	57%	77.7%	99.4%
SAU802400	BPT100841	31%	35.8%	68.6%
SAU802400	BCE101590	33%	70.4%	75.8%
SAU802400	BFU104746	33%	99.3%	93.3%
SAU802400	BMA109485	49%	97.8%	97.2%
SAU802400	CAC102162	30%	48.6%	97.1%
SAU802400	CBO101506	28%	45.8%	89.0%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802400	CDF102934	28%	48.7%	45.6%
SAU802400	EBC103870	35%	99.0%	95.2%
SAU802400	ECO103288	35%	99.0%	95.2%
SAU802400	KPN300216	41%	12.2%	79.4%
SAU802400	KPN303469	33%	99.4%	97.1%
SAU802400	MCA101622	28%	41.4%	71.9%
SAU802400	MAV102348	33%	93.4%	91.2%
SAU802400	MBV104807	33%	97.8%	82.6%
SAU802400	MTU200251	33%	98.0%	93.4%
SAU802400	PRT105408	35%	99.4%	95.0%
SAU802400	PAE201780	48%	99.5%	98.8%
SAU802400	PPU107970	33%	94.6%	90.1%
SAU802400	PSY104967	34%	94.3%	79.7%
SAU802400	SPA103178	36%	39.0%	65.3%
SAU802400	STY101426	35%	99.5%	95.4%
SAU802400	STM102828	35%	99.0%	95.2%
SAU802400	SAU802400	100%	100%	100%
SAU802400	SEP201017	82%	100%	100%
SAU802400	SHA101602	84%	99.8%	100%
SAU802400	YPS001671	34%	99.4%	95.0%
SAU802401	BAN101769	25%	49.4%	73.3%
SAU802401	BAN106436	21%	88.1%	91.1%
SAU802401	BAN106118	20%	97.9%	95.2%
SAU802401	BAN109894	27%	96.7%	97.9%
SAU802401	BCE113179	19%	49.8%	96.9%
SAU802401	BFU104281	25%	42.0%	78.2%
SAU802401	BMA108024	20%	41.6%	80.5%
SAU802401	MAV101627	25%	85.2%	86.1%
SAU802401	SAU802401	100%	100%	100%
SAU802401	SEP201019	55%	98.4%	100%
SAU802401	SHA101601	49%	97.5%	98.7%
SAU802401	YPS002784	31%	33.3%	9.3%
SAU802418	LPN101927	20%	49.1%	32.6%
SAU802418	PSY104376	28%	21.0%	32.1%
SAU802418	SAU802418	100%	100%	100%
SAU802418	SAU800111	28%	37.9%	49.8%
SAU802418	VCH101393	28%	19.6%	14.9%
SAU802419	BAN101272	21%	87.1%	89.5%
SAU802419	BAN107130	21%	88.3%	89.9%
SAU802419	SAU801819	33%	89.0%	84.9%
SAU802419	SAU802421	29%	98.1%	95.4%
SAU802419	SAU802004	29%	92.2%	91.1%
SAU802419	SAU801163	25%	95.5%	96.9%
SAU802419	SAU802005	34%	87.4%	77.8%
SAU802419	SAU802420	67%	98.4%	99.0%
SAU802419	SAU801820	70%	98.4%	99.0%
SAU802419	SAU802419	100%	100%	100%
SAU802425	ABA100387	33%	89.9%	91.8%
SAU802425	BAN102051	49%	94.3%	96.9%
SAU802425	BAN104523	52%	94.3%	95.2%
SAU802425	BPT101142	33%	87.5%	87.4%
SAU802425	BCE111317	34%	82.1%	78.5%
SAU802425	BFU107999	31%	95.2%	87.6%
SAU802425	BMA105033	33%	88.7%	87.9%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802425	CJU101589	33%	80.3%	97.1%
SAU802425	CPN200793	31%	89.3%	90.9%
SAU802425	CAC101689	37%	94.3%	97.3%
SAU802425	CBO100552	37%	93.4%	97.5%
SAU802425	CDF101504	38%	94.6%	98.5%
SAU802425	CDP101447	34%	93.4%	94.9%
SAU802425	EBC101268	33%	85.1%	86.8%
SAU802425	ECO100751	33%	85.1%	83.5%
SAU802425	HIN101001	30%	85.7%	86.5%
SAU802425	HPY101386	30%	80.3%	96.8%
SAU802425	KPN301793	33%	89.0%	87.3%
SAU802425	LPN101546	35%	84.8%	90.3%
SAU802425	MCA102956	34%	90.1%	89.3%
SAU802425	MAV100547	33%	92.2%	79.9%
SAU802425	MBV101758	32%	92.2%	85.2%
SAU802425	MLP100755	33%	92.2%	89.9%
SAU802425	MTU201568	32%	92.2%	89.1%
SAU802425	NGO100345	29%	80.3%	77.4%
SAU802425	NME201245	30%	82.1%	79.4%
SAU802425	PMU100379	31%	88.4%	88.7%
SAU802425	PRT105537	33%	85.1%	83.8%
SAU802425	PAE200499	31%	90.7%	86.4%
SAU802425	PPU105080	33%	83.3%	79.8%
SAU802425	PSY103312	33%	83.6%	80.1%
SAU802425	SPA100245	33%	71.3%	92.7%
SAU802425	STY102313	34%	85.1%	83.5%
SAU802425	STM102072	34%	85.1%	83.5%
SAU802425	SAU802425	100%	100%	100%
SAU802425	SEP202217	77%	94.9%	99.1%
SAU802425	SHA101398	76%	94.9%	99.1%
SAU802425	VCH101093	33%	83.9%	80.9%
SAU802425	YPS002123	31%	85.1%	83.8%
SAU802426	ABA100566	35%	94.5%	95.5%
SAU802426	BAN105329	49%	97.3%	100%
SAU802426	BAN100374	50%	99.1%	97.2%
SAU802426	BFR105798	33%	96.9%	55.9%
SAU802426	BPT100802	34%	92.0%	97.4%
SAU802426	BBU100339	31%	10.4%	17.5%
SAU802426	BCE102714	33%	94.7%	93.3%
SAU802426	BCE101562	34%	93.4%	95.3%
SAU802426	BFU107996	33%	92.7%	91.4%
SAU802426	BMA105498	36%	83.2%	80.2%
SAU802426	CJU100276	35%	96.9%	99.1%
SAU802426	CPN200796	35%	93.8%	94.8%
SAU802426	CAC103102	39%	98.5%	99.8%
SAU802426	CDP101053	30%	97.8%	96.3%
SAU802426	ECO100750	32%	96.5%	96.7%
SAU802426	HIN101523	33%	95.6%	95.8%
SAU802426	HPY100960	36%	96.7%	97.0%
SAU802426	KPN301795	32%	96.5%	95.4%
SAU802426	MCA100377	35%	96.0%	94.1%
SAU802426	MAV103992	34%	92.9%	87.7%
SAU802426	MBV102582	32%	92.9%	91.5%
SAU802426	MLP100752	34%	83.8%	84.9%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802426	MTU201547	32%	92.9%	91.5%
SAU802426	NGO101913	35%	88.1%	93.1%
SAU802426	NME200866	35%	92.9%	92.4%
SAU802426	PMU101900	33%	95.8%	88.2%
SAU802426	PRT101762	35%	96.2%	97.4%
SAU802426	PAE200419	39%	96.5%	93.4%
SAU802426	PPU109348	37%	98.2%	83.1%
SAU802426	PSY103605	37%	98.2%	94.9%
SAU802426	STY102312	33%	96.5%	96.7%
SAU802426	SAU802426	100%	100%	100%
SAU802426	SEP200097	76%	99.8%	100%
SAU802426	VCH101092	33%	96.2%	96.7%
SAU802426	YPS002121	36%	91.6%	93.1%
SAU802439	BCE107747	30%	77.0%	98.2%
SAU802439	CAC103752	23%	19.5%	31.6%
SAU802439	CBO102950	23%	64.9%	85.5%
SAU802439	CDP101057	24%	61.1%	75.2%
SAU802439	MBV101962	28%	60.7%	73.6%
SAU802439	MTU202253	28%	60.7%	73.6%
SAU802439	NGO101840	24%	44.9%	52.8%
SAU802439	SAU802439	100%	100%	100%
SAU802439	SHA101133	63%	99.3%	99.0%
SAU802439	SPN400573	25%	98.3%	96.3%
SAU802439	SPY101946	37%	28.5%	92.9%
SAU802442	BFU112290	35%	18.0%	17.2%
SAU802442	BFU101947	40%	22.3%	20.2%
SAU802442	EBC101408	25%	85.5%	85.0%
SAU802442	KPN302715	26%	56.2%	51.2%
SAU802442	LPN102898	25%	61.1%	36.1%
SAU802442	PRT102223	25%	86.2%	86.1%
SAU802442	SAU802442	100%	100%	100%
SAU802442	SHA102938	79%	100%	100%
SAU802442	VCH101669	25%	60.1%	61.2%
SAU802444	MGE100123	21%	24.2%	33.3%
SAU802444	SAU802444	100%	100%	100%
SAU802444	SEP201112	80%	100%	100%
SAU802444	SHA101626	68%	98.9%	98.9%
SAU802448	BFR102635	36%	85.4%	86.0%
SAU802448	BPT102384	34%	86.1%	83.6%
SAU802448	BCE102560	46%	72.0%	77.3%
SAU802448	BFU103281	42%	88.3%	90.8%
SAU802448	BMA103809	50%	55.4%	72.8%
SAU802448	CAC100655	43%	88.8%	96.6%
SAU802448	CBO102037	44%	88.8%	94.3%
SAU802448	CDF102723	47%	88.8%	96.6%
SAU802448	CDP101406	52%	58.5%	87.7%
SAU802448	EBC101184	41%	88.3%	97.9%
SAU802448	EFA200443	60%	93.9%	98.7%
SAU802448	EFM101077	34%	90%	98.2%
SAU802448	ECO102088	43%	73.2%	98.7%
SAU802448	KPN308726	40%	75.1%	99.0%
SAU802448	LMO100952	61%	94.9%	98.2%
SAU802448	MAV103175	38%	88.8%	98.1%
SAU802448	MBV105820	39%	88.0%	95.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802448	MTU203703	39%	88.0%	95.2%
SAU802448	PRT102695	32%	84.4%	87.2%
SAU802448	PAE203888	40%	88.3%	94.1%
SAU802448	PPU103929	43%	87.8%	93.5%
SAU802448	PSY108132	43%	87.8%	93.5%
SAU802448	SPA101282	41%	73.2%	96.5%
SAU802448	STY104336	41%	88.3%	95.5%
SAU802448	STM103203	35%	84.4%	87%
SAU802448	SAU802448	100%	100%	100%
SAU802448	SEP201147	78%	98.8%	97.6%
SAU802448	SHA100819	76%	99.8%	86.4%
SAU802448	SMU101306	56%	91.0%	97.4%
SAU802448	SPY100277	34%	79.3%	98.3%
SAU802448	YPS000240	45%	73.2%	97.8%
SAU802452	ABA103825	24%	94.4%	90.3%
SAU802452	BAN112396	28%	25.6%	73.2%
SAU802452	BAN105354	34%	44.6%	95.1%
SAU802452	BAN111201	29%	90.6%	89.7%
SAU802452	BFR104989	19%	90.9%	90.8%
SAU802452	BPT100181	24%	93.7%	92.4%
SAU802452	BCE102642	28%	95.2%	88.5%
SAU802452	BFU108139	27%	89.1%	88.4%
SAU802452	BMA102629	27%	94.7%	93.8%
SAU802452	CJU101166	25%	98.7%	97.2%
SAU802452	CDP100795	20%	95.4%	88.3%
SAU802452	EBC101460	25%	85.3%	95.4%
SAU802452	EFA200778	28%	95.4%	93.7%
SAU802452	ECO101499	26%	94.9%	92.4%
SAU802452	HIN100128	24%	94.7%	92.7%
SAU802452	HPY101168	26%	97.0%	94.9%
SAU802452	KPN301059	26%	95.4%	94.4%
SAU802452	LPN100988	24%	89.4%	89.5%
SAU802452	LMO100724	26%	97.0%	97.4%
SAU802452	MAV104012	23%	90.9%	86.5%
SAU802452	MBV102693	21%	89.1%	89.3%
SAU802452	MTU200190	21%	93.4%	89.3%
SAU802452	NGO102033	20%	95.2%	99.2%
SAU802452	PMU100949	25%	94.9%	90.6%
SAU802452	PRT100064	26%	95.4%	82.5%
SAU802452	PAE203301	32%	91.4%	90.3%
SAU802452	PPU111526	25%	95.2%	95.6%
SAU802452	PSY101770	25%	95.2%	94.8%
SAU802452	SPA101640	26%	96.2%	96.4%
SAU802452	STY104274	26%	94.9%	92.4%
SAU802452	STM103712	26%	96.2%	95.4%
SAU802452	SAU802452	100%	100%	100%
SAU802452	SEP201161	77%	98.7%	99.5%
SAU802452	SHA101184	72%	98.7%	99.7%
SAU802452	YPS002886	29%	94.7%	94.8%
SAU802459	ABA104623	35%	97.1%	85.3%
SAU802459	BAN110218	39%	91.4%	94.1%
SAU802459	BAN106937	47%	96%	96.6%
SAU802459	BPT100094	34%	92.6%	79.8%
SAU802459	BCE110085	36%	96.2%	85.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802459	BFU101558	35%	95.0%	86.9%
SAU802459	BMA107414	37%	95.0%	88.2%
SAU802459	CDF100518	31%	28.8%	86.1%
SAU802459	CDF103659	31%	64.6%	66.9%
SAU802459	LPN101703	36%	93.9%	87.2%
SAU802459	MCA101185	35%	98.5%	87.7%
SAU802459	PAE203600	36%	94.7%	86.2%
SAU802459	PPU110002	36%	93.0%	81.8%
SAU802459	SAU802459	100%	100%	100%
SAU802459	SEP200972	78%	100%	100%
SAU802459	SHA101719	75%	99.8%	99.6%
SAU802464	PRT104892	41%	97.0%	97.8%
SAU802464	SAU802464	100%	100%	100%
SAU802464	SEP200047	69%	98.9%	98.9%
SAU802467	ABA100843	20%	73.5%	75.7%
SAU802467	BAN108463	24%	64.8%	70%
SAU802467	BAN105979	26%	93.6%	93.1%
SAU802467	BPT102300	26%	79.9%	78.2%
SAU802467	BCE113024	27%	65.0%	72.8%
SAU802467	BFU100703	27%	94.4%	94.6%
SAU802467	BMA100152	25%	23.5%	45.6%
SAU802467	BMA105680	27%	72.6%	74.3%
SAU802467	CJU101490	27%	91.9%	93.2%
SAU802467	CBO100751	24%	96.1%	95.3%
SAU802467	CBO101097	23%	95.9%	95.1%
SAU802467	CBO101308	25%	92.7%	88.8%
SAU802467	CDF101830	20%	96.1%	95.4%
SAU802467	CDF101269	25%	91.0%	89.3%
SAU802467	CDP100600	27%	55.5%	51.7%
SAU802467	EBC100767	25%	95.3%	96.6%
SAU802467	ECO103399	34%	93.2%	94.3%
SAU802467	HIN100833	22%	93.2%	93.3%
SAU802467	HPY100294	25%	89.1%	87.1%
SAU802467	KPN300173	48%	16.0%	77.0%
SAU802467	KPN304736	31%	93.0%	94.4%
SAU802467	LPN103438	24%	59.2%	79.0%
SAU802467	LMO100125	23%	92.7%	92.0%
SAU802467	MAV103759	24%	77.3%	79.2%
SAU802467	MLP100689	20%	76.9%	78.1%
SAU802467	PMU100236	25%	96.4%	96.4%
SAU802467	PRT101741	41%	94.4%	95.0%
SAU802467	PAE204498	24%	94.7%	94.7%
SAU802467	PAE204494	25%	84.2%	84.5%
SAU802467	PPU106604	34%	93.0%	99.2%
SAU802467	PSY102116	26%	85.9%	84.7%
SAU802467	SPA102842	26%	90.2%	94.6%
SAU802467	STY100765	26%	95.3%	96.6%
SAU802467	SAU802467	100%	100%	100%
SAU802467	SEP200050	82%	100%	100%
SAU802467	SHA102504	27%	97.6%	96.7%
SAU802467	SHA102341	28%	95.7%	95.4%
SAU802467	SPY201537	27%	76.5%	74.4%
SAU802467	VCH100169	26%	75.4%	70.3%
SAU802467	YPS002641	26%	85.2%	85.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802468	PAE204830	31%	96.5%	94.7%
SAU802468	SAU802468	100%	100%	100%
SAU802468	SEP200060	61%	98.4%	99.1%
SAU802468	YPS001170	29%	91.2%	91.7%
SAU802469	PAE204831	25%	84.6%	87.1%
SAU802469	SAU802469	100%	100%	100%
SAU802469	SEP200061	62%	99.3%	99.6%
SAU802469	YPS001169	28%	65.8%	67.9%
SAU802472	BFR11509	39%	90.8%	98.0%
SAU802472	BPT101439	41%	93.0%	98.8%
SAU802472	BFU103591	40%	93.0%	89.8%
SAU802472	CAC101364	36%	92.6%	94.8%
SAU802472	CDF100553	36%	92.3%	94.7%
SAU802472	EFA200981	37%	93.8%	95.9%
SAU802472	EFA201256	36%	93.0%	95.0%
SAU802472	EFM202362	37%	93.8%	95.9%
SAU802472	KPN103715	36%	91.5%	98.4%
SAU802472	MAV106724	36%	91.2%	95.7%
SAU802472	MBV102804	39%	93.4%	98.0%
SAU802472	MLP100673	29%	84.9%	83.0%
SAU802472	MTU201908	39%	93.4%	98.0%
SAU802472	PAE201648	39%	93.0%	98.8%
SAU802472	PPU101577	35%	94.9%	95.8%
SAU802472	SAU802472	100%	100%	100%
SAU802472	SEP200975	76%	99.3%	99.3%
SAU802472	SHA101724	77%	100%	100%
SAU802472	SPN400290	35%	92.6%	93.4%
SAU802472	SPY200457	35%	93.8%	97.0%
SAU802472	VCH101567	37%	93.4%	96.8%
SAU802473	BFR12135	33%	93.8%	98.8%
SAU802473	BPT101434	22%	72.9%	85.3%
SAU802473	CTR100501	44%	9.2%	7.8%
SAU802473	CDF101113	40%	97.5%	100%
SAU802473	CDF103684	41%	99.4%	98.6%
SAU802473	CDP101707	32%	88.7%	98.1%
SAU802473	EBC100434	33%	71.5%	91.4%
SAU802473	EFA201330	27%	27.0%	26.8%
SAU802473	ECO101307	35%	95.3%	94.9%
SAU802473	KPN304537	36%	95.3%	95.3%
SAU802473	MCA101881	37%	98.2%	94.0%
SAU802473	NGO100614	37%	97.1%	97.3%
SAU802473	NME201822	37%	97.1%	97.3%
SAU802473	PMU101104	37%	99.4%	98.9%
SAU802473	PRT100243	37%	97.3%	98.5%
SAU802473	SAU802473	100%	100%	100%
SAU802473	SHA101725	74%	99.4%	99.2%
SAU802473	SPY200100	23%	65.6%	68.3%
SAU802473	VCH100864	36%	99.2%	97.0%
SAU802473	YPS001074	31%	95.5%	95.2%
SAU802481	CBO103036	28%	47.0%	37.8%
SAU802481	SAU802486	82%	97.3%	100%
SAU802481	SAU802481	100%	100%	100%
SAU802481	SEP200591	74%	88.3%	98.7%
SAU802481	SEP200552	71%	97.7%	98.9%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802481	SEP200589	73%	98.1%	99.2%
SAU802481	SEP200598	60%	87.9%	99.1%
SAU802481	SEP200593	62%	87.5%	97.1%
SAU802481	SEP200083	59%	93.6%	99.6%
SAU802481	SEP200597	60%	97.7%	99.2%
SAU802481	SEP200616	60%	97.7%	99.6%
SAU802481	SEP200553	66%	97.0%	98.8%
SAU802481	SHA101524	83%	67.8%	98.4%
SAU802488	ABA100783	23%	17.9%	16.1%
SAU802488	ABA100144	24%	19.8%	17.3%
SAU802488	EBC102917	30%	19.8%	16.7%
SAU802488	ECO102143	32%	19.8%	16.7%
SAU802488	HPY101500	34%	52.2%	39.5%
SAU802488	HPY100585	21%	69.2%	34.5%
SAU802488	KPN301786	31%	20.6%	17.5%
SAU802488	PRT101141	36%	15.5%	13.1%
SAU802488	STY104333	31%	19.8%	16.7%
SAU802488	STM100155	31%	19.8%	16.7%
SAU802488	SAU802488	100%	100%	100%
SAU802488	SEP201002	64%	99.8%	52.0%
SAU802488	SPY101669	29%	20.4%	22.5%
SAU802488	YPS000334	33%	20.0%	16.1%
SAU802491	BAN105883	33%	91.6%	96.2%
SAU802491	BAN103235	39%	91.6%	96.5%
SAU802491	BFR101582	36%	90.7%	93.3%
SAU802491	BBU100834	32%	87.8%	92.3%
SAU802491	BFU111711	22%	84.2%	75.5%
SAU802491	BFU102625	22%	84.2%	85.9%
SAU802491	CPN200707	34%	85.2%	85.1%
SAU802491	CTR200560	33%	85.9%	86.0%
SAU802491	CAC102619	37%	89.4%	92.7%
SAU802491	CBO103621	39%	90.6%	93.9%
SAU802491	CDF104307	34%	92.6%	97.0%
SAU802491	CDF100956	35%	96.6%	95.5%
SAU802491	CDP101629	32%	88.2%	90%
SAU802491	EFA200367	40%	91.9%	96.7%
SAU802491	EFM101685	35%	93.1%	97.6%
SAU802491	HIN100721	32%	82.7%	94.2%
SAU802491	LMO102655	38%	91.6%	96.2%
SAU802491	MAV100233	28%	91.9%	96.2%
SAU802491	MBV100850	29%	90.7%	94.8%
SAU802491	MLP100433	28%	91.1%	94.6%
SAU802491	MTU203265	29%	90.7%	94.8%
SAU802491	MGE100053	29%	90.4%	94%
SAU802491	MPN100088	28%	86.1%	89.4%
SAU802491	PMU101074	33%	88.9%	89.8%
SAU802491	PRT100549	22%	84.2%	87.8%
SAU802491	PPU110293	23%	84.2%	88.3%
SAU802491	PSY105678	24%	87.7%	91.1%
SAU802491	STM101606	22%	84.6%	88.3%
SAU802491	SAU802491	100%	100%	100%
SAU802491	SEP201006	66%	93.1%	99.6%
SAU802491	SHA102495	55%	93.3%	99.3%
SAU802491	SMU100294	38%	88.0%	92.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802491	SPN401350	36%	87.1%	91.6%
SAU802491	SPY200938	38%	88.0%	92.5%
SAU802491	TPA100634	33%	89.4%	92.5%
SAU802491	UUR100536	29%	88.2%	90.8%
SAU802491	VCH103757	33%	90.1%	93.7%
SAU802496	BMA100689	34%	8.4%	10.3%
SAU802496	CBO102378	29%	5.3%	29.8%
SAU802496	CDF100714	32%	10.1%	26.9%
SAU802496	CDF102419	29%	44.8%	45.1%
SAU802496	SAU802496	100%	100%	100%
SAU802496	SEP202577	60%	93.0%	4.9%
SAU802496	SHA102996	55%	71.4%	76.9%
SAU802496	SPN401042	23%	95.4%	20.8%
SAU802496	SPN400581	26%	83.4%	22.3%
SAU802496	SPY100688	30%	13.5%	21.7%
SAU802496	UUR100377	20%	56%	71.6%
SAU802502	ABA105088	40%	11.7%	31.9%
SAU802502	BAN109365	16%	27.4%	32.3%
SAU802502	BAN100965	21%	29.1%	17.2%
SAU802502	BAN111001	19%	23.2%	12.6%
SAU802502	BPT105763	30%	12.2%	37.3%
SAU802502	BPT105804	40%	5.2%	14.2%
SAU802502	BBU100545	16%	19.0%	70.6%
SAU802502	BCE111297	41%	13.5%	13.5%
SAU802502	BFU107405	42%	8.1%	53.4%
SAU802502	BMA109637	37%	6.1%	59.8%
SAU802502	CJU101536	29%	12.2%	50.7%
SAU802502	CPN200033	19%	22.1%	25.6%
SAU802502	CPN200268	39%	7.8%	8.9%
SAU802502	CTR200876	22%	8.8%	35.4%
SAU802502	CDF103752	27%	8.8%	56.4%
SAU802502	CDF102641	30%	38.5%	41.7%
SAU802502	CDP102558	27%	9.3%	7.8%
SAU802502	CDP101521	30%	8.9%	13.9%
SAU802502	EBC100323	28%	11.8%	45.4%
SAU802502	EFA201300	46%	9.9%	47.8%
SAU802502	EFA200083	45%	15.1%	90.2%
SAU802502	EFA202388	39%	18.2%	85.1%
SAU802502	EFA203524	21%	28.8%	44.4%
SAU802502	EFA200038	42%	64.3%	66.7%
SAU802502	EFM201584	29%	21.7%	36.8%
SAU802502	ECO102908	34%	5.8%	10.4%
SAU802502	ECO101223	36%	6.9%	23.4%
SAU802502	HPY101323	29%	13.4%	43.9%
SAU802502	HPY100575	31%	12.5%	31.5%
SAU802502	KPN201031	32%	11.8%	21.2%
SAU802502	LPN101461	21%	18.3%	52.1%
SAU802502	LMO101802	34%	15.1%	29.1%
SAU802502	LMO101963	29%	15.3%	35.8%
SAU802502	MCA102006	28%	4.7%	25.8%
SAU802502	MBV106185	38%	9.9%	24.2%
SAU802502	MLP100033	28%	11.1%	25.8%
SAU802502	MTU203821	33%	10.8%	9.5%
SAU802502	MTU203824	37%	10.3%	25.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802502	MGE100323	22%	25.8%	53.4%
SAU802502	MPN100275	27%	88.8%	52.7%
SAU802502	MPN100388	29%	8.2%	55.8%
SAU802502	NGO100382	20%	17.2%	36.2%
SAU802502	NGO101515	20%	17.2%	50%
SAU802502	NGO100447	20%	17.2%	36.2%
SAU802502	NGO101440	20%	17.2%	36.2%
SAU802502	NGO101563	29%	13.4%	19.4%
SAU802502	NME201654	22%	17.3%	29.3%
SAU802502	NME200717	30%	8.4%	15.5%
SAU802502	PMU100098	28%	66.5%	29.9%
SAU802502	PRT100444	30%	5.7%	49.5%
SAU802502	PRT105010	39%	13.0%	38.3%
SAU802502	PAE203113	27%	10.0%	10.8%
SAU802502	PAE200196	41%	7.3%	39.6%
SAU802502	PPU102161	31%	8.9%	42.4%
SAU802502	PSY102683	33%	8.1%	6.7%
SAU802502	PSY104998	41%	11.2%	15.8%
SAU802502	SPA103530	23%	14.6%	48.9%
SAU802502	STY101188	24%	14.6%	49.1%
SAU802502	SAU800563	19%	99.4%	98.2%
SAU802502	SAU802630	21%	90.4%	65.7%
SAU802502	SAU800561	21%	99.4%	98.0%
SAU802502	SAU800811	22%	99.7%	99.4%
SAU802502	SAU802503	66%	100%	100%
SAU802502	SAU802502	100%	100%	100%
SAU802502	SEP200110	20%	96.6%	87.8%
SAU802502	SHA100540	23%	15.7%	88.6%
SAU802502	SHA102998	24%	18.9%	71.5%
SAU802502	SHA100562	23%	78.7%	84.7%
SAU802502	SMU100238	40%	14.6%	19.7%
SAU802502	SMU100747	22%	19.7%	29.2%
SAU802502	SMU100749	44%	6.5%	5.8%
SAU802502	SPN401402	39%	66.8%	88.1%
SAU802502	SPY201545	29%	62.2%	35.1%
SAU802502	TPA100365	33%	12.2%	17.4%
SAU802502	VCH100756	50%	2.3%	7.7%
SAU802502	YPS002256	39%	5.0%	22.1%
SAU802503	ABA105088	30%	11.0%	40.3%
SAU802503	BAN109365	16%	27.2%	34.7%
SAU802503	BAN111001	19%	74.9%	41.9%
SAU802503	BPT105763	24%	3.8%	23.5%
SAU802503	BPT105804	41%	13.4%	14.1%
SAU802503	BBU100545	25%	12.1%	45.8%
SAU802503	BCE111297	45%	13.3%	16.6%
SAU802503	BFU107405	45%	10.2%	78.4%
SAU802503	BMA109637	50%	2.6%	47.5%
SAU802503	CJU101103	22%	35.8%	64.9%
SAU802503	CPN200033	19%	17.5%	22.0%
SAU802503	CPN200268	34%	6.0%	8.5%
SAU802503	CTR200876	33%	13.4%	40.4%
SAU802503	CBO103272	23%	28.7%	56.4%
SAU802503	CDF103752	27%	13.1%	53.5%
SAU802503	CDF102641	29%	7.6%	12.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802503	CDP101521	33%	11.9%	6.8%
SAU802503	EBC103874	27%	16.6%	39.4%
SAU802503	EBC100323	29%	7.4%	52.7%
SAU802503	EFA202388	52%	10.0%	47.9%
SAU802503	EFA200083	50%	14.3%	29.1%
SAU802503	EFA201300	48%	16.7%	89.6%
SAU802503	EFA200038	37%	59.2%	87.4%
SAU802503	EFM201584	28%	16.1%	49.4%
SAU802503	ECO102908	37%	8.2%	9.8%
SAU802503	ECO103311	24%	94.5%	35.7%
SAU802503	ECO101223	40%	7.9%	29.7%
SAU802503	HPY101323	32%	11.7%	53.0%
SAU802503	HPY100575	31%	14.4%	55.2%
SAU802503	KPN201031	24%	12.0%	39.9%
SAU802503	LPN101461	24%	12.8%	43.5%
SAU802503	LMO101963	31%	6.4%	27.1%
SAU802503	LMO101802	34%	15.7%	29.3%
SAU802503	MCA102006	40%	6.6%	26.1%
SAU802503	MBV106185	39%	10.3%	27.8%
SAU802503	MLP100033	28%	6.1%	23.5%
SAU802503	MTU203824	38%	9.5%	21.8%
SAU802503	MTU203821	37%	11.8%	50.6%
SAU802503	MGE100323	21%	21.9%	55.8%
SAU802503	MPN100275	23%	22.8%	15.5%
SAU802503	MPN100388	27%	12.0%	55.1%
SAU802503	NGO101440	20%	15.9%	36.2%
SAU802503	NGO101515	20%	15.9%	50%
SAU802503	NGO100447	20%	15.9%	36.2%
SAU802503	NGO100382	20%	15.9%	36.2%
SAU802503	NGO101563	28%	9.8%	17.0%
SAU802503	NME201654	22%	21.8%	36.7%
SAU802503	NME200717	31%	8.1%	13.7%
SAU802503	PMU100098	28%	92.6%	35.8%
SAU802503	PRT105010	36%	14.7%	38.3%
SAU802503	PRT100444	35%	6.0%	35.4%
SAU802503	PAE203113	25%	9.6%	10.9%
SAU802503	PAE200196	36%	6.3%	45.9%
SAU802503	PPU102161	33%	5.3%	40.3%
SAU802503	PSY108790	31%	6.9%	4.8%
SAU802503	PSY102683	43%	10.2%	6.7%
SAU802503	PSY104998	37%	11.4%	31.5%
SAU802503	SPA103530	22%	17.7%	47.7%
SAU802503	STY101188	22%	16.6%	52.1%
SAU802503	SAU802630	20%	99.3%	97.9%
SAU802503	SAU800561	21%	99.4%	98.0%
SAU802503	SAU800563	20%	99.4%	98.2%
SAU802503	SAU800811	22%	85.1%	96.7%
SAU802503	SAU802502	65%	100%	100%
SAU802503	SAU802503	100%	100%	100%
SAU802503	SEP200110	20%	95.6%	92.8%
SAU802503	SHA100540	21%	16.3%	85.1%
SAU802503	SHA100562	23%	17.3%	15.2%
SAU802503	SHA102998	23%	18.5%	71.8%
SAU802503	SMU100238	23%	19.0%	33.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802503	SMU100747	21%	37.7%	61.4%
SAU802503	SMU100749	40%	14.5%	6.5%
SAU802503	SPN401402	39%	4.8%	4.0%
SAU802503	SPY201545	34%	13.5%	19.3%
SAU802503	TPA100365	35%	14.0%	17.4%
SAU802503	VCH100756	58%	5.7%	5.9%
SAU802503	YPS002256	38%	9.8%	5.9%
SAU802506	BAN112425	42%	97.9%	100%
SAU802506	BAN111510	60%	98.3%	98.8%
SAU802506	BFR11473	25%	74.9%	77.2%
SAU802506	BCE101565	30%	95.9%	96.6%
SAU802506	BFU100630	27%	89.9%	85.9%
SAU802506	BMA108610	28%	95.9%	98.1%
SAU802506	CAC102691	31%	97.7%	99.8%
SAU802506	CDF101648	31%	96.9%	97.3%
SAU802506	EBC104555	27%	95.2%	98.6%
SAU802506	EFA200809	39%	98.1%	99.6%
SAU802506	EFM202150	36%	98.5%	100%
SAU802506	ECO103486	25%	95.2%	98.6%
SAU802506	HIN101086	24%	87.6%	87.9%
SAU802506	KPN309070	26%	87.0%	90.1%
SAU802506	LMO101414	41%	98.1%	98.0%
SAU802506	PMU101371	25%	94.4%	98.6%
SAU802506	PRT101395	25%	94.4%	97.7%
SAU802506	STY100699	26%	95.2%	98.6%
SAU802506	STM104115	22%	93.6%	96.4%
SAU802506	SAU802506	100%	100%	100%
SAU802506	SEP201009	76%	99.2%	100%
SAU802506	SHA100834	81%	98.8%	99.8%
SAU802506	YPS000393	27%	97.7%	99.2%
SAU802507	ABA101570	30%	61.9%	56.1%
SAU802507	BAN111763	36%	85.8%	81.1%
SAU802507	BAN106500	46%	100%	93.0%
SAU802507	BPT103130	25%	83.6%	87.7%
SAU802507	BCE107345	29%	61.1%	57.7%
SAU802507	BFU100176	21%	88.5%	74.8%
SAU802507	BFU104257	27%	61.5%	52.8%
SAU802507	BFU103403	21%	88.1%	78.9%
SAU802507	CAC102025	23%	78.8%	81.5%
SAU802507	CDF104417	31%	64.2%	65.8%
SAU802507	CDF100440	27%	81.9%	76.1%
SAU802507	CDP100432	25%	81.9%	83.3%
SAU802507	EBC103251	22%	88.1%	85.5%
SAU802507	EFA200682	32%	31.9%	31.6%
SAU802507	ECO101511	22%	87.6%	85.1%
SAU802507	KPN306069	23%	87.6%	85.1%
SAU802507	MAV104574	32%	23.0%	21.2%
SAU802507	MAV103382	25%	66.4%	61.6%
SAU802507	MAV101336	24%	87.2%	84.1%
SAU802507	MBV102645	25%	57.5%	49.4%
SAU802507	MTU200164	25%	57.5%	49.6%
SAU802507	PRT100638	20%	92.5%	94.1%
SAU802507	PAE200796	21%	93.4%	87.5%
SAU802507	PPU106554	26%	63.3%	66.1%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802507	PSY105573	22%	84.5%	78.5%
SAU802507	SPA101683	21%	79.6%	60.2%
SAU802507	STY104298	22%	88.1%	85.5%
SAU802507	STM104445	21%	79.6%	60.2%
SAU802507	SAU802507	100%	100%	100%
SAU802507	SEP201029	73%	99.6%	99.6%
SAU802507	SHA100833	74%	98.2%	96.9%
SAU802507	SMU100140	23%	61.5%	61.1%
SAU802507	SPY102945	32%	21.7%	52.5%
SAU802507	VCH101315	25%	82.3%	92.3%
SAU802507	YPS003104	24%	54.4%	56.4%
SAU802510	BAN101366	23%	53.1%	26.2%
SAU802510	BMA100274	45%	21.6%	60.3%
SAU802510	CBO102568	26%	64.8%	13.5%
SAU802510	CBO100474	28%	78.4%	16.5%
SAU802510	EFA200549	40%	40.7%	44%
SAU802510	EFM100539	43%	40.7%	44.6%
SAU802510	LMO102593	50%	32.7%	91.4%
SAU802510	PAE201642	28%	73.5%	36.3%
SAU802510	SAU802510	100%	100%	100%
SAU802510	SEP201035	34%	84.6%	99.3%
SAU802510	SHA100027	51%	43.2%	63.1%
SAU802511	ABA101187	32%	25.0%	21.5%
SAU802511	BPT102628	28%	28.3%	30.1%
SAU802511	BCE107041	29%	25.0%	28.6%
SAU802511	BFU102753	24%	32.3%	21.7%
SAU802511	BMA106189	21%	72.7%	66.9%
SAU802511	CJU100519	28%	29.0%	8.0%
SAU802511	EBC103859	24%	43.3%	75.1%
SAU802511	EFA200764	23%	28.2%	49.1%
SAU802511	EFA200374	31%	26.9%	46.2%
SAU802511	ECO103281	23%	92.6%	85.6%
SAU802511	HIN101645	21%	93.9%	85.8%
SAU802511	KPN301327	21%	92.6%	86.1%
SAU802511	LPN101554	19%	43.7%	77.7%
SAU802511	LPN103586	22%	39.7%	88.8%
SAU802511	MCA100529	35%	8.9%	15.0%
SAU802511	MAV101852	23%	27.3%	21.9%
SAU802511	NGO101970	21%	65.2%	63.7%
SAU802511	NME200209	20%	66.7%	64.4%
SAU802511	PMU100392	21%	90.1%	84.2%
SAU802511	PRT101407	24%	51.7%	44.9%
SAU802511	PAE203303	21%	20.4%	19.4%
SAU802511	PAE201269	20%	23.4%	21.6%
SAU802511	PPU109268	24%	33.1%	29.4%
SAU802511	PSY101807	21%	22.9%	21.1%
SAU802511	SPA103296	23%	52.4%	48.6%
SAU802511	STY103605	29%	24.4%	20.2%
SAU802511	STM102815	22%	98.2%	91.9%
SAU802511	SAU802511	100%	100%	100%
SAU802511	SEP201036	61%	99.3%	94.8%
SAU802511	SHA101790	61%	85.7%	98.3%
SAU802511	VCH103439	27%	28.5%	23.4%
SAU802511	YPS001766	19%	85.5%	79.0%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802518	ABA105593	29%	50.8%	39.2%
SAU802518	BAN110972	45%	82.2%	91.6%
SAU802518	BAN100218	45%	93.4%	91.6%
SAU802518	BBU100645	26%	63.5%	35.5%
SAU802518	BCE107415	21%	88.8%	81.5%
SAU802518	BFU112947	22%	98.5%	92.7%
SAU802518	CTR100655	27%	58.4%	45.2%
SAU802518	CDF100729	25%	58.9%	39.1%
SAU802518	EFA201235	55%	93.4%	92%
SAU802518	EFM200131	42%	93.4%	91.5%
SAU802518	LPN100583	24%	74.1%	73.5%
SAU802518	LMO102230	42%	93.4%	92.1%
SAU802518	PAE200542	26%	82.7%	51.9%
SAU802518	PPU111804	30%	52.3%	52.8%
SAU802518	PSY105127	30%	80.2%	69.2%
SAU802518	SAU802518	100%	100%	100%
SAU802518	SHA101221	72%	86.3%	98.3%
SAU802520	BAN108403	43%	71.5%	100%
SAU802520	BAN112352	46%	91.7%	89.2%
SAU802520	BFR105372	33%	52.8%	70%
SAU802520	BPT102354	27%	75%	65.3%
SAU802520	BFU110972	30%	77.8%	66.5%
SAU802520	BMA102527	28%	51.4%	46.2%
SAU802520	CAC103017	25%	95.8%	90.3%
SAU802520	CDP101090	30%	79.2%	86.0%
SAU802520	EBC101510	27%	75.7%	63.1%
SAU802520	EFA201241	44%	97.9%	99.3%
SAU802520	EFM101277	27%	52.8%	49.7%
SAU802520	ECO102629	28%	75.7%	63.1%
SAU802520	KPN304419	27%	75.7%	63.1%
SAU802520	LMO100103	26%	79.9%	81.2%
SAU802520	MBV101633	28%	54.2%	48.5%
SAU802520	MLP101283	22%	69.4%	69.9%
SAU802520	MTU200734	28%	54.2%	48.5%
SAU802520	PRT102689	28%	77.8%	65.1%
SAU802520	STY102739	28%	75.7%	63.1%
SAU802520	STM103221	28%	75.7%	63.1%
SAU802520	SAU802520	100%	100%	100%
SAU802520	SHA100070	77%	100%	100%
SAU802520	SMU101475	31%	92.4%	89.3%
SAU802520	SPN401598	26%	82.6%	89.4%
SAU802520	SPY201508	36%	90.3%	91.5%
SAU802520	YPS002793	28%	75.7%	65.3%
SAU802522	ABA102625	29%	25%	23.0%
SAU802522	BAN101372	31%	86.9%	84.3%
SAU802522	BAN110637	34%	86.9%	81.6%
SAU802522	BCE111951	27%	42.9%	36.2%
SAU802522	BFU108797	23%	79.1%	60.2%
SAU802522	EFA201248	39%	40.3%	94.0%
SAU802522	KPN303068	30%	46.6%	40.9%
SAU802522	LMO101465	38%	92.9%	90.7%
SAU802522	PRT103713	24%	42.9%	93.7%
SAU802522	PAE203501	28%	47.0%	60.2%
SAU802522	PPU109159	25%	43.7%	91.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802522	SPA100901	26%	42.9%	94.6%
SAU802522	STM103633	26%	42.9%	94.6%
SAU802522	SAU802522	100%	100%	100%
SAU802522	SEP201068	61%	96.6%	97.7%
SAU802522	SHA100686	63%	77.6%	99.0%
SAU802522	SPN400066	34%	81.7%	77.1%
SAU802522	SPY201605	32%	89.2%	83.9%
SAU802528	BAN103721	26%	97.1%	97.6%
SAU802528	CAC100274	29%	89.3%	91.2%
SAU802528	CDP100640	26%	66.5%	50.2%
SAU802528	CDP101493	34%	36.9%	22.5%
SAU802528	CDP100638	26%	67.5%	41.2%
SAU802528	CDP101495	40%	36.4%	23.4%
SAU802528	CDP100684	31%	64.1%	45.0%
SAU802528	EFA202035	28%	70.4%	58.2%
SAU802528	EFM200204	23%	92.7%	57.4%
SAU802528	LMO101005	27%	88.3%	86.0%
SAU802528	SAU802528	100%	100%	100%
SAU802528	SEP201093	71%	99.5%	99.5%
SAU802528	SHA102510	79%	99.5%	99.5%
SAU802528	SMU100891	28%	59.7%	50.4%
SAU802528	SPN300435	33%	59.2%	43.1%
SAU802528	SPY200880	27%	88.8%	78.7%
SAU802539	BFR102568	31%	95.9%	95.7%
SAU802539	BCE113546	30%	96.2%	94.4%
SAU802539	BFU115336	32%	93.3%	87.7%
SAU802539	BFU112943	33%	93.3%	93.3%
SAU802539	BMA108339	31%	96.4%	97.2%
SAU802539	CDP100580	30%	95.0%	95.2%
SAU802539	EBC102312	33%	94.6%	96.1%
SAU802539	EFM100662	36%	91.2%	100%
SAU802539	ECO100847	33%	94.6%	95.5%
SAU802539	KPN301806	33%	94.6%	95.5%
SAU802539	LMO100148	57%	100%	100%
SAU802539	MAV104239	33%	92.9%	92.8%
SAU802539	PRT102417	31%	98.1%	98.8%
SAU802539	PAE202106	34%	93.1%	94.1%
SAU802539	PSY105421	30%	94.6%	95.6%
SAU802539	STY102871	32%	94.6%	95.5%
SAU802539	SAU802539	100%	100%	100%
SAU802539	SEP201171	84%	100%	100%
SAU802539	SHA102199	81%	100%	100%
SAU802539	SPN400642	31%	97.9%	96.6%
SAU802539	YPS001186	32%	94.6%	95.5%
SAU802545	BBU100684	34%	91.8%	87.9%
SAU802545	BCE107302	50%	37.9%	82.1%
SAU802545	BMA103982	27%	23.1%	54.0%
SAU802545	EFM100738	56%	37.6%	100%
SAU802545	LPN103488	35%	99.1%	96.8%
SAU802545	LMO100989	41%	100%	99.8%
SAU802545	PAE110993	24%	48.9%	30.6%
SAU802545	SAU802545	100%	100%	100%
SAU802545	SEP201177	81%	99.8%	99.8%
SAU802545	SHA101318	82%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802545	SMU100946	44%	96.5%	99.8%
SAU802545	SPN401568	42%	97.9%	98.1%
SAU802545	SPY200655	43%	96.7%	96%
SAU802547	ABA105572	39%	90.8%	97.5%
SAU802547	BAN101922	36%	76.3%	90.4%
SAU802547	BAN104869	42%	90.8%	98%
SAU802547	BFR100765	43%	71.1%	68.0%
SAU802547	BPT103019	37%	86.7%	77.9%
SAU802547	BCE103848	40%	89.6%	88.7%
SAU802547	BFU110234	38%	86.7%	64.2%
SAU802547	BMA101458	44%	26.0%	71.4%
SAU802547	BMA108546	39%	60.7%	27.5%
SAU802547	CJU100775	36%	91.9%	98.7%
SAU802547	CPN200150	30%	64.7%	60.7%
SAU802547	CTR200751	26%	48.0%	43.9%
SAU802547	CAC103117	37%	88.4%	92.9%
SAU802547	CBO100820	33%	87.3%	92.3%
SAU802547	CDF100241	49%	97.1%	97.2%
SAU802547	CDP100500	32%	69.9%	83.7%
SAU802547	EBC100683	45%	60.7%	60.1%
SAU802547	EFA201894	37%	65.9%	65.0%
SAU802547	EFM201553	37%	87.3%	96.7%
SAU802547	ECO101306	43%	60.7%	59.1%
SAU802547	HIN100382	46%	98.8%	87.9%
SAU802547	HPY100668	37%	90.2%	88.1%
SAU802547	KPN302255	39%	74.6%	36.6%
SAU802547	LPN100954	37%	88.4%	92.3%
SAU802547	LMO102205	33%	90.8%	46.6%
SAU802547	MCA101470	41%	65.9%	55.8%
SAU802547	MAV102898	41%	90.8%	92.1%
SAU802547	MBV100407	44%	86.7%	88.5%
SAU802547	MLP100717	44%	86.7%	88.5%
SAU802547	MTU201299	44%	86.7%	88.5%
SAU802547	NGO100306	42%	61.8%	35.3%
SAU802547	NME201587	41%	61.8%	35.3%
SAU802547	PMU101068	44%	98.3%	95.6%
SAU802547	PRT106182	32%	93.1%	99.4%
SAU802547	PAE200994	36%	86.7%	86.7%
SAU802547	PPU110616	38%	86.1%	89.2%
SAU802547	PSY102798	40%	54.9%	40.5%
SAU802547	SPA102006	41%	59.0%	57.3%
SAU802547	STY103674	42%	59.0%	57.3%
SAU802547	STM100933	42%	59.0%	57.3%
SAU802547	SAU802547	100%	100%	100%
SAU802547	SEP201179	60%	98.8%	99.4%
SAU802547	SHA101314	58%	100%	100%
SAU802547	SMU101210	42%	93.1%	98.2%
SAU802547	SPN401316	40%	97.1%	96.0%
SAU802547	TPA100140	36%	57.8%	53.7%
SAU802547	VCH103735	40%	90.8%	98.1%
SAU802547	YPS001868	43%	59.0%	57.0%
SAU802548	SPA102343	38%	93.6%	82.7%
SAU802548	STM102687	38%	93.6%	80.2%
SAU802548	SAU802548	100%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802548	SMU100972	64%	98.6%	98.1%
SAU802548	SPN400307	62%	100%	99.9%
SAU802548	SPY200663	63%	98.6%	97.9%
SAU802555	ABA106035	32%	54.3%	54.2%
SAU802555	BAN106994	48%	40.7%	95.3%
SAU802555	BFR11792	51%	93.5%	95.4%
SAU802555	BCE103747	41%	82.4%	88.6%
SAU802555	BFU112906	30%	53.8%	51.9%
SAU802555	CJU100202	33%	45.7%	40.7%
SAU802555	CPN200095	27%	50.3%	30.8%
SAU802555	CTR200807	31%	50.3%	30.7%
SAU802555	CAC101718	48%	94.0%	91.2%
SAU802555	CBO101588	44%	94.0%	84.5%
SAU802555	CDF103080	40%	92.0%	98.9%
SAU802555	CDF103398	47%	93.0%	99.5%
SAU802555	CDP101537	45%	65.3%	92.3%
SAU802555	EBC103982	40%	91.5%	98.4%
SAU802555	EFA204780	39%	99.5%	69.8%
SAU802555	EFM202301	33%	84.4%	95.8%
SAU802555	ECO100334	42%	93.5%	91.1%
SAU802555	KPN303887	40%	91.5%	95.7%
SAU802555	LMO101588	39%	92.5%	96.8%
SAU802555	MAV101369	34%	56.3%	42.5%
SAU802555	MBV105847	36%	56.3%	30.7%
SAU802555	MLP101056	34%	55.8%	43.7%
SAU802555	MTU202994	36%	56.3%	36%
SAU802555	NGO101296	43%	54.3%	62.2%
SAU802555	NME200459	42%	54.3%	62.9%
SAU802555	PMU101056	44%	92.5%	90.6%
SAU802555	PPU102678	38%	87.4%	96.1%
SAU802555	PSY104038	36%	56.3%	31.0%
SAU802555	SPA100218	40%	91.5%	98.4%
SAU802555	STY100785	40%	91.5%	98.4%
SAU802555	SAU802555	100%	100%	100%
SAU802555	SHA101210	67%	95.0%	99.0%
SAU802555	SPN300070	41%	92.0%	97.3%
SAU802555	SPY200807	56%	93.5%	98.9%
SAU802555	VCH103556	34%	97.0%	97.9%
SAU802557	ABA101879	45%	97.9%	97.7%
SAU802557	BAN105978	59%	60.2%	99.8%
SAU802557	BAN110321	61%	70.9%	100%
SAU802557	BFR10291	40%	0.9%	8.6%
SAU802557	BPT102136	43%	4.2%	12.6%
SAU802557	BCE110602	45%	75.2%	97.9%
SAU802557	BFU101728	44%	90.5%	96.7%
SAU802557	BMA106854	46%	74.8%	73.3%
SAU802557	CJU101080	31%	93.1%	92.9%
SAU802557	CPN200982	31%	82.0%	93.6%
SAU802557	CTR200100	30%	82.0%	97.0%
SAU802557	CAC100879	48%	17.1%	8.6%
SAU802557	CBO102754	47%	16.6%	8.1%
SAU802557	CDF102644	49%	98.3%	98.6%
SAU802557	CDP100778	43%	0.4%	9.2%
SAU802557	EBC104530	46%	78.9%	95.9%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802557	EFA201855	49%	8.1%	16.4%
SAU802557	EFM201092	51%	1.4%	7.8%
SAU802557	ECO100475	38%	99.5%	99.9%
SAU802557	HIN100276	37%	0.4%	9.3%
SAU802557	HPY101055	37%	1.5%	7.8%
SAU802557	KPN308679	39%	97.3%	100%
SAU802557	LPN101141	45%	78.9%	88.6%
SAU802557	LPN101253	45%	78.9%	88.3%
SAU802557	LMO100878	51%	1.1%	8.3%
SAU802557	MCA100406	38%	0.9%	8.6%
SAU802557	MAV100988	33%	88.0%	95.4%
SAU802557	MBV103852	51%	75.7%	76.1%
SAU802557	MLP101210	43%	79.9%	84.5%
SAU802557	MTU200960	51%	75.7%	78.3%
SAU802557	MGE100073	25%	62.8%	66.7%
SAU802557	MPN100622	25%	67.5%	69.6%
SAU802557	NGO100160	39%	0.2%	9.7%
SAU802557	NME201398	39%	0.2%	9.7%
SAU802557	PMU101892	39%	0.7%	8.8%
SAU802557	PRT105848	44%	99.0%	98.6%
SAU802557	PAE203917	43%	98.9%	99.5%
SAU802557	PPU108258	44%	7.9%	16.1%
SAU802557	PSY102170	44%	0.1%	9.1%
SAU802557	SPA101217	38%	89.3%	100%
SAU802557	STY100871	38%	99.5%	99.9%
SAU802557	STM104228	45%	0.7%	8.0%
SAU802557	SAU802557	100%	100%	100%
SAU802557	SEP201193	73%	99.1%	100%
SAU802557	SHA100292	69%	76.4%	100%
SAU802557	SMU100795	45%	1.0%	8.4%
SAU802557	SPN400641	45%	81.2%	86.5%
SAU802557	SPY201317	43%	1.4%	8.0%
SAU802557	TPA101026	35%	89.9%	99.2%
SAU802557	UUR100203	31%	80.2%	94.5%
SAU802557	VCH102181	42%	5.2%	5.5%
SAU802557	YPS001578	40%	8.4%	17.0%
SAU802558	BAN109810	45%	83.8%	98.3%
SAU802558	BFU109224	40%	88.2%	72.2%
SAU802558	EBC100081	41%	88.2%	75%
SAU802558	EFM202554	38%	86.8%	85.5%
SAU802558	HIN100277	42%	89.7%	88.2%
SAU802558	HIN100278	42%	89.7%	88.2%
SAU802558	HPY101056	32%	89.7%	90.9%
SAU802558	KPN304604	38%	88.2%	65.9%
SAU802558	LMO102528	41%	98.5%	98.5%
SAU802558	MCA101196	42%	97.1%	94.3%
SAU802558	MAV101708	32%	89.7%	85.7%
SAU802558	NGO102035	40%	97.1%	94.3%
SAU802558	PMU101891	47%	98.5%	95.7%
SAU802558	PPU102427	41%	91.2%	90.8%
SAU802558	PSY107623	37%	91.2%	90.8%
SAU802558	SPA101034	40%	63.2%	59.5%
SAU802558	SAU802558	100%	100%	100%
SAU802558	SEP201194	61%	98.5%	94.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802558	SHA101777	62%	98.5%	98.5%
SAU802558	UUR100202	24%	95.6%	86.5%
SAU802564	BAN107558	26%	29.2%	33.1%
SAU802564	BAN112682	21%	44.5%	43.9%
SAU802564	BAN101794	21%	44.5%	44.1%
SAU802564	BMA102467	36%	8.9%	44.4%
SAU802564	LMO100571	26%	99.2%	98.6%
SAU802564	PAE200420	24%	54.3%	48.0%
SAU802564	SAU802564	100%	100%	100%
SAU802564	SHA101771	69%	99.0%	98.0%
SAU802565	SAU802565	100%	100%	100%
SAU802565	SHA103208	47%	41.2%	88.3%
SAU802567	BFU100798	25%	57.2%	94.4%
SAU802567	BMA109603	32%	58.2%	48.1%
SAU802567	CTR200330	25%	16.3%	20.0%
SAU802567	EFM201158	21%	29.5%	65.2%
SAU802567	ECO203243	27%	18.4%	30.2%
SAU802567	HIN100372	29%	36.5%	89.8%
SAU802567	KPN206582	24%	60.7%	96.5%
SAU802567	LPN100851	30%	13.9%	19.0%
SAU802567	LPN101642	31%	62.0%	53.8%
SAU802567	LMO102084	41%	96.7%	98.7%
SAU802567	MAV107021	31%	61.7%	94.2%
SAU802567	MBV105112	33%	57.9%	58.8%
SAU802567	MLP101575	34%	61.9%	59.2%
SAU802567	MTU200111	34%	61.9%	57.5%
SAU802567	NGO101829	27%	95.0%	96.1%
SAU802567	PRT104518	30%	57.7%	51.1%
SAU802567	PAE203155	33%	56.7%	51.4%
SAU802567	PPU103844	22%	57.4%	93.3%
SAU802567	SPA103154	31%	58.2%	53.0%
SAU802567	STY101087	30%	58.2%	53.0%
SAU802567	SAU802567	100%	100%	100%
SAU802567	SEP201198	64%	98.8%	99.2%
SAU802567	SMU101308	26%	95.5%	97.0%
SAU802567	SPN401865	26%	95.2%	97.2%
SAU802567	SPY200033	26%	95.2%	96.8%
SAU802580	BFR10064	24%	86.6%	86.0%
SAU802580	BPT100834	33%	82.1%	85.3%
SAU802580	BCE103008	24%	73.8%	70.3%
SAU802580	BFU100508	22%	69.6%	67.3%
SAU802580	BFU104873	25%	83.9%	70.6%
SAU802580	BFU103585	28%	82.4%	74.7%
SAU802580	BFU103576	29%	73.5%	67.0%
SAU802580	KPN302051	31%	76.5%	79.8%
SAU802580	LPN102617	32%	83.0%	82.9%
SAU802580	LMO102915	42%	98.8%	100%
SAU802580	MAV103755	39%	98.2%	99.4%
SAU802580	MBV100078	24%	71.4%	73.0%
SAU802580	MTU203462	24%	71.4%	73.0%
SAU802580	SAU802580	100%	100%	100%
SAU802580	SHA101214	73%	69.0%	100%
SAU802581	BAN101204	26%	48.9%	56.7%
SAU802581	BAN103460	27%	93.5%	90.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802581	BFU105217	23%	43.8%	39.6%
SAU802581	BFU103369	23%	43.8%	39.5%
SAU802581	CDF100605	26%	57.2%	55.6%
SAU802581	CDF103586	25%	48.6%	52.0%
SAU802581	LMO101378	66%	100%	100%
SAU802581	MAV108594	30%	44.6%	39.1%
SAU802581	SAU802581	100%	100%	100%
SAU802581	SHA102890	70%	99.6%	99.6%
SAU802581	SMU100172	31%	46.7%	34.9%
SAU802581	TPA100942	26%	42.0%	33.3%
SAU802585	BAN105638	33%	58.2%	61.8%
SAU802585	BAN113350	30%	75.5%	87.8%
SAU802585	BAN112732	30%	75.5%	87.8%
SAU802585	CAC102695	34%	89.8%	66.4%
SAU802585	CAC101396	34%	89.8%	66.4%
SAU802585	SAU802585	100%	100%	100%
SAU802585	SEP200238	78%	100%	100%
SAU802586	CBO101009	37%	38.5%	3.6%
SAU802586	EFA102043	24%	80.3%	84.2%
SAU802586	SAU802586	100%	100%	100%
SAU802587	SAU802587	100%	100%	100%
SAU802590	SAU802590	100%	100%	100%
SAU802590	SEP201225	49%	93.4%	86.7%
SAU802599	ABA105729	42%	97.1%	100%
SAU802599	BAN109585	45%	96.7%	96.1%
SAU802599	BAN103122	55%	96.7%	95.3%
SAU802599	BFR101138	43%	94.9%	95.6%
SAU802599	BPT102100	38%	91.5%	89.9%
SAU802599	BCE108792	39%	94.9%	95.6%
SAU802599	BFU102636	39%	94.9%	95.6%
SAU802599	BMA109222	39%	94.9%	95.6%
SAU802599	CJU100267	47%	95.2%	94.9%
SAU802599	CAC102467	44%	97.8%	98.2%
SAU802599	CBO102096	47%	95.2%	95.3%
SAU802599	CDF100322	43%	94.9%	94.9%
SAU802599	CDP101560	40%	77.9%	100%
SAU802599	EBC103390	44%	94.9%	98.1%
SAU802599	EFA200426	50%	93.0%	93.1%
SAU802599	EFM200299	50%	93.0%	93.1%
SAU802599	ECO100134	44%	94.9%	98.1%
SAU802599	HPY101041	39%	93.0%	94.1%
SAU802599	KPN305802	45%	94.9%	98.1%
SAU802599	LMO101566	54%	92.3%	91.7%
SAU802599	MCA100866	39%	94.9%	93.9%
SAU802599	MAV103092	43%	92.3%	88.8%
SAU802599	MBV104454	44%	90.1%	87.9%
SAU802599	MLP100998	42%	92.3%	88.5%
SAU802599	MTU202191	44%	90.1%	87.9%
SAU802599	NGO101061	42%	95.6%	99.2%
SAU802599	NME201002	42%	95.6%	99.2%
SAU802599	PRT102516	42%	94.9%	98.1%
SAU802599	PAE204725	41%	94.9%	97.7%
SAU802599	PPU108442	41%	94.9%	92.9%
SAU802599	PSY105156	42%	94.9%	97.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802599	SPA104023	39%	94.9%	97.7%
SAU802599	STY103388	43%	94.9%	97.7%
SAU802599	SAU802599	100%	100%	100%
SAU802599	SEP201249	75%	100%	100%
SAU802599	SHA101527	74%	100%	100%
SAU802599	VCH100581	40%	94.5%	97.7%
SAU802599	YPS000790	46%	95.2%	98.1%
SAU802601	EBC102039	34%	77.8%	87.6%
SAU802601	EFM100783	70%	20.5%	73.8%
SAU802601	KPN304221	32%	99.1%	89.6%
SAU802601	SAU802601	100%	100%	100%
SAU802601	SMU100354	42%	99.6%	99.2%
SAU802601	SPN401248	42%	98.3%	95.9%
SAU802601	SPY101115	40%	47.4%	92%
SAU802601	VCH101565	30%	98.3%	88.1%
SAU802605	BCE111163	23%	63.8%	65.2%
SAU802605	EFA202884	32%	42.8%	28.2%
SAU802605	SAU802605	100%	100%	100%
SAU802605	SEP201630	47%	97.8%	94.4%
SAU802605	SHA103206	40%	93.5%	91.5%
SAU802605	YPS004171	25%	52.9%	56.5%
SAU802606	LPN100635	28%	61.1%	53.0%
SAU802606	MAV102533	61%	98.6%	98.7%
SAU802606	STY101723	32%	15.5%	12.4%
SAU802606	SAU802606	100%	100%	100%
SAU802606	SEP201634	92%	100%	100%
SAU802606	SHA101827	93%	44.3%	100%
SAU802610	BAN105148	30%	61.9%	56.1%
SAU802610	BAN112430	33%	61.9%	54.5%
SAU802610	BFU101996	28%	51.0%	63.1%
SAU802610	CBO103389	30%	37.4%	54.9%
SAU802610	CDP101315	23%	55.8%	80.2%
SAU802610	LMO101650	18%	56.5%	49.1%
SAU802610	MAV100914	23%	46.9%	90.8%
SAU802610	MBV100112	23%	63.3%	88.6%
SAU802610	MLP101168	25%	53.7%	75.2%
SAU802610	MTU203540	23%	63.3%	88.6%
SAU802610	PRT104693	25%	53.7%	52.3%
SAU802610	SAU802610	100%	100%	100%
SAU802610	SEP203908	63%	99.3%	98.6%
SAU802610	SHA101334	65%	99.3%	93.6%
SAU802612	ABA105055	52%	95.8%	98.9%
SAU802612	BPT101787	34%	75.6%	97.9%
SAU802612	BCE100989	49%	86.5%	95.0%
SAU802612	BFU106253	51%	94.0%	95.0%
SAU802612	BMA100271	50%	95.8%	96.1%
SAU802612	CJU100383	29%	13.5%	13.8%
SAU802612	CDP100617	62%	96.3%	92.1%
SAU802612	EBC100717	53%	48.2%	94.8%
SAU802612	ECO100303	49%	95.4%	97.7%
SAU802612	KPN300102	52%	24.4%	100%
SAU802612	KPN304388	50%	96.0%	98.6%
SAU802612	MAV102913	33%	94.0%	99.4%
SAU802612	MBV105546	37%	93.0%	98.9%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802612	MTU201262	37%	93.0%	98.9%
SAU802612	PRT102375	50%	96.0%	98.4%
SAU802612	PAE205367	49%	96.5%	97.9%
SAU802612	PPU102034	51%	96.5%	97.2%
SAU802612	PSY102763	51%	96.0%	96.1%
SAU802612	SAU802612	100%	100%	100%
SAU802612	SEP201650	88%	99.6%	99.5%
SAU802612	SHA101538	89%	99.6%	99.5%
SAU802612	YPS002162	52%	96.0%	96.3%
SAU802613	ABA104044	41%	95.0%	95.9%
SAU802613	BAN108237	36%	95.8%	93.5%
SAU802613	BAN113091	41%	96.0%	97.3%
SAU802613	BAN112735	41%	96.8%	96.4%
SAU802613	BAN113417	44%	96.0%	95.5%
SAU802613	BFR103003	30%	23.8%	85.5%
SAU802613	BFU102984	38%	97.6%	98.4%
SAU802613	BFU103241	39%	97.4%	94.1%
SAU802613	BFU100165	42%	96.6%	98.8%
SAU802613	BMA103749	40%	96.0%	88.6%
SAU802613	CJU100455	34%	79.2%	99.5%
SAU802613	CAC103154	33%	96.0%	97.5%
SAU802613	CDP100607	51%	97.6%	94.3%
SAU802613	EBC101625	41%	95.6%	96.5%
SAU802613	ECO100304	41%	95.6%	96.5%
SAU802613	KPN304386	40%	95.6%	96.5%
SAU802613	LPN101129	47%	97.8%	99.2%
SAU802613	LMO102125	39%	96.6%	97.3%
SAU802613	MCA100475	37%	95.8%	94.2%
SAU802613	MAV101782	41%	94.8%	94.0%
SAU802613	MAV103466	41%	94.8%	93.0%
SAU802613	MLP101520	30%	90.3%	96.9%
SAU802613	NGO100472	36%	91.3%	91.4%
SAU802613	NME200446	36%	96.0%	98.5%
SAU802613	PPU109546	42%	95.4%	95.5%
SAU802613	PSY103463	41%	95.6%	96.5%
SAU802613	SPA103863	35%	95.4%	97.3%
SAU802613	STY103756	38%	95.0%	96.7%
SAU802613	SAU802613	100%	100%	100%
SAU802613	SEP201652	89%	100%	100%
SAU802613	SHA101537	87%	100%	100%
SAU802613	SMU101316	31%	91.3%	97.4%
SAU802613	SPY200809	30%	91.7%	96.1%
SAU802613	YPS002165	40%	95.6%	96.5%
SAU802627	BAN110806	44%	75.1%	96.9%
SAU802627	BAN110948	47%	98.9%	96.7%
SAU802627	BFR101036	31%	88.6%	94.0%
SAU802627	BCE114143	31%	88.6%	91.7%
SAU802627	BMA108016	31%	88.6%	75.0%
SAU802627	CAC102470	23%	36.5%	49.1%
SAU802627	EBC102822	37%	64.1%	75.4%
SAU802627	EFA202089	46%	97.0%	95.5%
SAU802627	ECO100375	36%	61.8%	69.0%
SAU802627	KPN304876	35%	72.4%	81.9%
SAU802627	PRT105117	33%	71.7%	78.1%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802627	PAE203294	37%	59.9%	69.7%
SAU802627	SAU802627	100%	100%	100%
SAU802627	SEP201696	66%	99.8%	98.2%
SAU802627	SHA101994	63%	99.8%	97.8%
SAU802627	YPS001866	36%	60.3%	69.4%
SAU802628	ABA105164	19%	63.7%	55.6%
SAU802628	ABA104704	17%	73.2%	74.7%
SAU802628	BAN106975	45%	82.2%	83.1%
SAU802628	BAN103536	45%	82.2%	83.1%
SAU802628	BFU101239	26%	65.0%	77.4%
SAU802628	BFU102576	25%	65.6%	77.0%
SAU802628	BMA109935	22%	73.2%	86.5%
SAU802628	CBO101313	29%	70.1%	75.9%
SAU802628	EBC103824	20%	68.2%	66.7%
SAU802628	EFA202071	20%	73.2%	80%
SAU802628	KPN300786	37%	33.1%	69.1%
SAU802628	LMO101624	44%	86.6%	92.1%
SAU802628	MAV105204	24%	70.1%	69.9%
SAU802628	PAE201652	36%	80.3%	82.3%
SAU802628	SPA102320	28%	59.2%	67.1%
SAU802628	STY100589	28%	59.2%	68.1%
SAU802628	STM104051	29%	59.2%	67.1%
SAU802628	SAU802628	100%	100%	100%
SAU802628	SEP201738	74%	94.3%	100%
SAU802628	SHA101864	73%	94.9%	100%
SAU802632	BFR105563	27%	32.0%	27.9%
SAU802632	BFU113817	42%	95.7%	99.0%
SAU802632	CBO100615	47%	95.7%	94.2%
SAU802632	EFA202434	54%	92.2%	94.5%
SAU802632	EFM201460	51%	96.3%	98.4%
SAU802632	LPN102484	27%	35.1%	32.9%
SAU802632	LMO102628	51%	96.6%	99.0%
SAU802632	PMU101896	29%	35.1%	32.4%
SAU802632	PRT105732	38%	95.7%	98.3%
SAU802632	SPA100561	39%	95.3%	98.3%
SAU802632	STM100668	39%	95.3%	98.3%
SAU802632	SAU802632	100%	100%	100%
SAU802632	SMU101540	48%	96.3%	98.4%
SAU802632	SPN200887	49%	81.1%	98.5%
SAU802632	SPY201189	49%	96.3%	98.4%
SAU802638	BAN107918	24%	65.7%	61.7%
SAU802638	SAU802638	100%	100%	100%
SAU802638	SEP202299	24%	72%	72.5%
SAU802638	SEP202175	32%	84%	89.4%
SAU802638	SHA100151	47%	100%	100%
SAU802641	BBU100407	43%	98.9%	3.7%
SAU802641	CPN200703	33%	19.7%	81.0%
SAU802641	CAC101724	45%	70.9%	98.7%
SAU802641	CDF103357	38%	99.2%	98.0%
SAU802641	EFM200703	52%	99.8%	99.7%
SAU802641	KPN103840	44%	46.6%	94.5%
SAU802641	MCA101148	20%	33.4%	75.1%
SAU802641	PMU101795	40%	22.8%	71.4%
SAU802641	SPA101839	42%	72.2%	87.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802641	SAU802641	100%	100%	100%
SAU802641	SEP201763	75%	100%	100%
SAU802641	VCH101790	30%	19.4%	84.9%
SAU802641	VCH101791	41%	5.4%	94.6%
SAU802641	VCH101792	40%	80.6%	5.2%
SAU802641	VCH101796	49%	99.5%	2.8%
SAU802642	BBU100406	35%	32.1%	26.6%
SAU802642	CAC102434	34%	98.7%	93.9%
SAU802642	CBO103509	30%	97.8%	92.9%
SAU802642	CDF100717	51%	98.7%	98.7%
SAU802642	CDP100913	29%	33.3%	28.0%
SAU802642	EFA201620	52%	99.4%	98.1%
SAU802642	EFM200644	52%	99.4%	98.4%
SAU802642	LMO100517	53%	99.4%	98.1%
SAU802642	MAV101383	33%	21.8%	17.4%
SAU802642	MBV104868	31%	22.4%	17.9%
SAU802642	MTU203212	31%	22.4%	17.9%
SAU802642	PMU100829	27%	30.8%	24%
SAU802642	SAU802642	100%	100%	100%
SAU802642	SEP201764	67%	99.0%	97.8%
SAU802642	SMU101180	54%	98.7%	97.5%
SAU802642	SPN400647	55%	99.0%	98.7%
SAU802642	SPY201392	53%	99.0%	97.5%
SAU802642	UUR100534	29%	26.6%	29.4%
SAU802642	VCH101797	33%	27.9%	23.7%
SAU802642	VCH100266	30%	28.2%	23.3%
SAU802642	YPS001750	27%	34.0%	28.1%
SAU802643	BAN103063	24%	97.3%	100%
SAU802643	BAN108458	30%	99.8%	99.8%
SAU802643	BFU109734	25%	33.9%	46.8%
SAU802643	CAC100500	26%	10.2%	46.0%
SAU802643	CBO100159	32%	0.5%	41.6%
SAU802643	CDF100068	36%	15.5%	91.1%
SAU802643	CDF103782	30%	0.4%	38.4%
SAU802643	CDP102624	20%	28.9%	62.2%
SAU802643	CDP101471	21%	95.0%	94.6%
SAU802643	CDP100399	22%	93.3%	90.2%
SAU802643	EFA200464	25%	99.8%	96.3%
SAU802643	EFM100294	34%	28.0%	94.6%
SAU802643	ECO103408	23%	16.5%	46.1%
SAU802643	HPY100285	27%	13.7%	4.5%
SAU802643	HPY100077	21%	7.4%	48.4%
SAU802643	HPY100225	22%	21.5%	45.8%
SAU802643	HPY101140	20%	62.3%	10.7%
SAU802643	HPY101226	22%	24.9%	32.5%
SAU802643	LMO102022	28%	99.8%	99.8%
SAU802643	MAV104113	21%	95.7%	94.0%
SAU802643	MLP101538	25%	17.0%	36.6%
SAU802643	PAE202571	19%	25.9%	45.6%
SAU802643	PSY103089	22%	24.1%	42.7%
SAU802643	SPA103375	26%	14.6%	21.8%
SAU802643	STY102351	21%	15.7%	44.6%
SAU802643	SAU802643	100%	100%	100%
SAU802643	SEP201765	66%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802643	SHA101169	63%	100%	100%
SAU802643	SMU101323	23%	96.8%	98.3%
SAU802643	SPN402036	27%	13.3%	54.1%
SAU802643	SPY201662	22%	96.8%	98.7%
SAU802643	YPS002077	25%	11.2%	47.6%
SAU802646	CTR100723	23%	21.7%	29.7%
SAU802646	SAU802646	100%	100%	100%
SAU802646	SEP201767	36%	98.1%	98.8%
SAU802646	SHA101749	33%	98.6%	98.1%
SAU802649	SAU802649	100%	100%	100%
SAU802649	SEP201787	64%	99.0%	99.0%
SAU802649	SHA102155	65%	100%	100%
SAU802649	SPN301641	44%	98.7%	99.1%
SAU802651	BAN102391	24%	20.3%	12.4%
SAU802651	EFA200259	31%	14.2%	25.1%
SAU802651	MAV106301	34%	13.8%	24.6%
SAU802651	SAU802651	100%	100%	100%
SAU802651	SEP201789	54%	99.4%	100%
SAU802651	SHA102153	56%	98.3%	98.7%
SAU802651	SPN301643	39%	98.3%	99.4%
SAU802651	SPY100103	44%	24.7%	100%
SAU802652	EBC103319	28%	17.0%	42.8%
SAU802652	MBV100249	23%	37.1%	54.4%
SAU802652	MTU201429	23%	37.1%	54.4%
SAU802652	SAU802652	100%	100%	100%
SAU802652	SEP201795	43%	99.2%	99.0%
SAU802652	SHA102150	41%	100%	100%
SAU802652	SPN301644	29%	98.8%	98.5%
SAU802652	SPY100024	44%	14.3%	39.9%
SAU802654	ABA105043	16%	61.1%	92.9%
SAU802654	BAN110387	21%	11.0%	67.1%
SAU802654	BAN112878	20%	60.3%	43.8%
SAU802654	BAN100594	20%	3.7%	27.2%
SAU802654	BAN103564	19%	7.7%	57.2%
SAU802654	BAN103966	20%	13.9%	37.7%
SAU802654	BAN106993	18%	11.8%	94.8%
SAU802654	BAN112238	17%	72.5%	19.9%
SAU802654	BFR100872	28%	49.2%	38.4%
SAU802654	BPT103725	21%	30.9%	38.8%
SAU802654	BCE107896	17%	6.2%	97.0%
SAU802654	BCE112211	26%	61.3%	91.7%
SAU802654	BCE114917	29%	18.7%	92.8%
SAU802654	BFU110407	15%	4.4%	99.1%
SAU802654	BFU101138	18%	91.2%	16.1%
SAU802654	BMA107841	21%	18.3%	94.5%
SAU802654	CJU101583	20%	14.5%	69.2%
SAU802654	CJU100590	20%	7.0%	88.4%
SAU802654	CPN200209	18%	10.4%	74.5%
SAU802654	CTR200684	21%	25.9%	74.6%
SAU802654	CTR200685	20%	4.0%	83.8%
SAU802654	CAC100010	16%	13.0%	98.6%
SAU802654	CBO100803	19%	39.0%	50.1%
SAU802654	CDF103991	17%	26.3%	87.2%
SAU802654	CDF104259	16%	16.8%	96.1%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802654	CDF102976	19%	30.9%	59.2%
SAU802654	CDF100770	18%	19.3%	66.5%
SAU802654	CDF100757	21%	37.3%	47.0%
SAU802654	CDF103200	17%	16.6%	86.6%
SAU802654	CDF100494	18%	24.5%	63.5%
SAU802654	CDF102075	18%	59.8%	95.2%
SAU802654	CDF100184	27%	15.1%	91.5%
SAU802654	CDF104552	17%	17.5%	88.7%
SAU802654	CDP102193	22%	14.6%	99.4%
SAU802654	EBC100399	19%	25.1%	67.8%
SAU802654	EBC100820	20%	54.4%	83.4%
SAU802654	EBC100805	17%	22.1%	98.2%
SAU802654	EBC101205	18%	15.9%	99.2%
SAU802654	EFA203174	27%	4.7%	40.4%
SAU802654	EFM202396	19%	13.4%	62.3%
SAU802654	EFM200591	19%	26.6%	67.6%
SAU802654	ECO101518	28%	35.1%	42.5%
SAU802654	ECO101343	20%	32.9%	86.5%
SAU802654	HIN100971	18%	37.6%	21.1%
SAU802654	HPY100603	15%	15.5%	17.9%
SAU802654	HPY100313	18%	12.1%	36.5%
SAU802654	HPY100602	19%	25.3%	48.7%
SAU802654	HPY101160	17%	18.5%	63.3%
SAU802654	HPY101226	17%	22.9%	56.8%
SAU802654	HPY100897	22%	1.2%	47.6%
SAU802654	HPY100077	22%	16.2%	65.0%
SAU802654	HPY100906	17%	59.6%	75.7%
SAU802654	HPY101140	19%	21.4%	43.5%
SAU802654	HPY100285	18%	86.7%	16.1%
SAU802654	KPN305221	17%	5.0%	25.9%
SAU802654	LPN102929	17%	12.8%	64.8%
SAU802654	LPN100835	19%	32.7%	84.0%
SAU802654	LPN102554	19%	22.0%	95.2%
SAU802654	LPN101177	19%	53.0%	83.2%
SAU802654	MCA100348	17%	58.9%	94.1%
SAU802654	MAV107352	19%	33.2%	95.6%
SAU802654	MBV103437	18%	40.3%	83.1%
SAU802654	MLP100263	27%	32.9%	48.3%
SAU802654	MTU201527	19%	20.0%	52.7%
SAU802654	MGE100347	16%	17.3%	20.7%
SAU802654	MPN100397	17%	11.0%	72.4%
SAU802654	NGO101220	16%	21.5%	66.1%
SAU802654	NME200634	18%	43.8%	46.9%
SAU802654	PMU100714	16%	13.2%	85.6%
SAU802654	PRT105107	16%	10.7%	92.9%
SAU802654	PAE201873	17%	66.9%	93.2%
SAU802654	PPU104136	17%	35.4%	37.4%
SAU802654	PSY108622	16%	73.8%	22.1%
SAU802654	PSY106453	19%	50.7%	87.8%
SAU802654	SPA103107	19%	25.2%	98.9%
SAU802654	STY100387	19%	26.4%	91.8%
SAU802654	STM104147	19%	6.4%	97.4%
SAU802654	SAU802654	100%	100%	100%
SAU802654	SEP201799	54%	98.8%	71.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802654	SHA102148	56%	10.7%	89.4%
SAU802654	SHA103225	61%	24.3%	97.0%
SAU802654	SPN301653	43%	94.5%	7.0%
SAU802654	SPY200509	16%	52.0%	89.0%
SAU802654	TPA100484	21%	27.1%	39.4%
SAU802654	YPS002407	18%	61.5%	83.5%
SAU802655	BFR105074	22%	73.9%	84.7%
SAU802655	BCE107142	38%	90%	96.2%
SAU802655	BFU100048	43%	89.1%	98.0%
SAU802655	EBC101089	38%	72.2%	100%
SAU802655	EFM102193	42%	46.5%	99.0%
SAU802655	KPN303589	43%	82.2%	87.7%
SAU802655	PPU103404	39%	90%	98.5%
SAU802655	PSY103942	41%	82.6%	87.0%
SAU802655	SAU802655	100%	100%	100%
SAU802655	SEP201777	93%	99.1%	99.6%
SAU802658	SAU802658	100%	100%	100%
SAU802658	SEP201781	72%	99.2%	100%
SAU802658	SHA100132	66%	100%	100%
SAU802662	BFR102810	23%	65.5%	68.1%
SAU802662	CAC101079	35%	78.8%	79.1%
SAU802662	CAC101508	33%	99.6%	99.2%
SAU802662	CBO100561	36%	78.8%	78.2%
SAU802662	EFM202294	43%	82.0%	82.7%
SAU802662	SAU802662	100%	100%	100%
SAU802681	CAC101008	23%	48.4%	63.1%
SAU802681	CDF102990	31%	19.3%	28.0%
SAU802681	EFM102460	38%	61.8%	99.2%
SAU802681	SAU802681	100%	100%	100%
SAU802681	SHA103018	64%	99.7%	100%
SAU802681	SPN300982	23%	20.9%	18.3%
SAU802686	CDF102022	36%	17.7%	18.1%
SAU802686	ECO204773	48%	97.9%	91.7%
SAU802686	HPY100700	49%	97.9%	91.7%
SAU802686	LMO101556	57%	97.2%	97.9%
SAU802686	SAU802686	100%	100%	100%
SAU802686	SMU100471	52%	97.9%	98.2%
SAU802686	SPN400428	53%	97.9%	94.8%
SAU802689	ABA104423	38%	71.7%	72.6%
SAU802689	BAN106956	65%	91.8%	93.6%
SAU802689	BAN108132	66%	94.7%	94.4%
SAU802689	BPT101446	35%	70.8%	93.4%
SAU802689	BCE111516	32%	56.6%	91.7%
SAU802689	BFU112966	31%	70.8%	73.7%
SAU802689	BMA107217	31%	71.7%	78.6%
SAU802689	CPN200011	35%	91.2%	89.2%
SAU802689	CTR200904	37%	92.8%	89.6%
SAU802689	CDP100811	35%	83.6%	88.8%
SAU802689	EBC101390	30%	88.1%	80.5%
SAU802689	EFA200985	75%	96.9%	97.5%
SAU802689	EFM201522	70%	97.2%	98.7%
SAU802689	ECO101028	32%	88.1%	80.3%
SAU802689	KPN300416	27%	34.6%	71.3%
SAU802689	KPN302517	32%	89.0%	80.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802689	LPN102475	44%	39.0%	97.7%
SAU802689	LMO100379	69%	96.5%	95.6%
SAU802689	PAE200857	37%	71.7%	72.8%
SAU802689	PPU109900	39%	71.7%	73.2%
SAU802689	PSY103191	39%	71.7%	71.6%
SAU802689	SPA101128	33%	65.7%	85.8%
SAU802689	STY102479	30%	88.1%	80.3%
SAU802689	STM102282	30%	88.1%	80.3%
SAU802689	SAU802689	100%	100%	100%
SAU802689	SEP202172	77%	99.7%	99.1%
SAU802689	SHA102497	82%	100%	99.4%
SAU802689	SPN400084	63%	95.9%	94.5%
SAU802689	SPY200686	64%	95.9%	94.5%
SAU802689	VCH101240	35%	72.3%	69.0%
SAU802689	YPS003127	31%	87.4%	78.6%
SAU802701	ABA102929	41%	87.3%	96.5%
SAU802701	BAN109528	29%	25.8%	95.5%
SAU802701	BAN100158	36%	38.5%	79.9%
SAU802701	BAN112678	26%	80.2%	78.6%
SAU802701	BAN110028	50%	40.9%	99.0%
SAU802701	BAN108206	48%	87.3%	22.2%
SAU802701	BAN101564	51%	69.8%	97.8%
SAU802701	BAN109552	43%	87.7%	95.7%
SAU802701	BAN111328	45%	97.2%	98.8%
SAU802701	BAN110379	47%	96.8%	96.8%
SAU802701	BAN108174	48%	97.2%	97.6%
SAU802701	BAN101135	49%	98.8%	100%
SAU802701	BAN112693	49%	100%	98.1%
SAU802701	BAN108774	51%	99.6%	97.7%
SAU802701	BCE101081	43%	86.5%	94.4%
SAU802701	BFU106323	40%	86.5%	72.9%
SAU802701	CAC100479	49%	100%	99.6%
SAU802701	CDF101638	49%	98.0%	99.2%
SAU802701	CDP101466	47%	81.0%	91.0%
SAU802701	EFA200808	49%	97.2%	96.1%
SAU802701	ECO100486	38%	87.7%	97.4%
SAU802701	KPN302594	39%	88.1%	95.7%
SAU802701	LMO102938	50%	99.6%	98.8%
SAU802701	MBV100633	36%	91.3%	93.1%
SAU802701	MTU200975	36%	91.3%	93.1%
SAU802701	MGE100067	45%	80.6%	43.1%
SAU802701	MPN100074	44%	80.6%	43.2%
SAU802701	PMU100448	41%	90.1%	96.9%
SAU802701	SPA101078	36%	80.2%	98.1%
SAU802701	SAU802701	100%	100%	100%
SAU802701	SEP201315	71%	100%	100%
SAU802701	SHA102331	72%	100%	100%
SAU802701	SPY201472	44%	94.4%	96.3%
SAU802701	VCH103502	39%	88.5%	98.7%
SAU802710	ABA100898	30%	79.1%	85.7%
SAU802710	BAN112555	58%	97.5%	100%
SAU802710	BAN106936	64%	98.7%	99.2%
SAU802710	BFR100717	35%	59.4%	66.5%
SAU802710	BPT103217	29%	67.4%	71.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802710	BBU100176	26%	72.0%	81.2%
SAU802710	BCE112346	30%	87.4%	89.9%
SAU802710	BFU105165	30%	84.5%	92.5%
SAU802710	BMA104306	30%	73.2%	76.3%
SAU802710	CJU100925	26%	68.2%	82.4%
SAU802710	CAC102710	43%	95.8%	96.2%
SAU802710	CBO101450	39%	93.3%	93.7%
SAU802710	CDF100026	49%	36.8%	88.1%
SAU802710	CDF104563	50%	89.1%	100%
SAU802710	CDP101653	40%	52.3%	59.2%
SAU802710	EBC100304	32%	78.2%	96.2%
SAU802710	EFA200737	62%	98.7%	99.6%
SAU802710	EFM200318	61%	98.7%	97.5%
SAU802710	ECO103661	34%	85.8%	93.7%
SAU802710	HIN100467	32%	87.4%	97.5%
SAU802710	HPY101046	33%	64.9%	83.7%
SAU802710	KPN301111	35%	87.4%	97.5%
SAU802710	LPN100764	33%	62.8%	69.2%
SAU802710	LMO101197	59%	98.7%	99.6%
SAU802710	MCA101113	31%	72.0%	76.9%
SAU802710	MAV100553	33%	49.8%	47.6%
SAU802710	MBV105240	32%	46.0%	48.7%
SAU802710	MLP101601	30%	69.5%	65.7%
SAU802710	MTU203864	31%	46.0%	48.7%
SAU802710	MGE100391	30%	62.8%	76.6%
SAU802710	MPN100284	28%	63.2%	77.5%
SAU802710	NGO100788	29%	84.5%	92.3%
SAU802710	NME200072	28%	84.9%	92.8%
SAU802710	PMU101486	34%	85.8%	92.4%
SAU802710	PRT105128	35%	74.1%	82.7%
SAU802710	PAE205559	28%	87.4%	93.0%
SAU802710	PPU102171	28%	89.5%	94.9%
SAU802710	PSY102503	29%	73.2%	79.0%
SAU802710	SPA103410	31%	89.1%	97.6%
SAU802710	STY103852	31%	89.1%	97.6%
SAU802710	SAU802710	100%	100%	100%
SAU802710	SEP201294	81%	99.6%	99.6%
SAU802710	SHA101597	82%	98.7%	98.3%
SAU802710	SMU100460	55%	98.7%	100%
SAU802710	SPN401163	53%	98.7%	96.7%
SAU802710	SPY200240	55%	98.7%	100%
SAU802710	TPA100936	27%	66.1%	70.7%
SAU802710	UUR100038	33%	88.7%	99.1%
SAU802710	VCH102735	32%	87.0%	94.3%
SAU802710	YPS000008	34%	83.7%	92.2%
SAU802711	ABA101587	49%	98.9%	98.6%
SAU802711	BAN106565	54%	99.0%	99.7%
SAU802711	BAN109722	76%	99.4%	98.7%
SAU802711	BFR10096	45%	97.6%	98.9%
SAU802711	BPT100036	48%	98.4%	97.8%
SAU802711	BBU100177	48%	98.6%	97.4%
SAU802711	BCE103020	47%	99.0%	96.2%
SAU802711	BFU109113	48%	98.4%	96.2%
SAU802711	BMA106271	48%	99.0%	96.0%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802711	CJU101113	46%	98.4%	99.4%
SAU802711	CPN200128	48%	98.1%	98.2%
SAU802711	CTR200774	47%	98.2%	98.5%
SAU802711	CAC101884	54%	98.1%	97.9%
SAU802711	CBO102626	55%	98.2%	97.0%
SAU802711	CDF103119	56%	98.2%	97.3%
SAU802711	EBC101931	52%	98.1%	99.0%
SAU802711	EFA200717	66%	99.4%	98.7%
SAU802711	EFM202552	66%	99.4%	98.4%
SAU802711	ECO103662	51%	98.9%	98.7%
SAU802711	HIN100562	50%	99.2%	99.0%
SAU802711	HPY100209	46%	99.0%	99.7%
SAU802711	KPN300377	54%	29.6%	93.4%
SAU802711	KPN301110	50%	95.4%	100%
SAU802711	LPN101818	49%	98.9%	99.0%
SAU802711	LMO102246	71%	99.2%	98.6%
SAU802711	MCA101156	47%	98.9%	97.6%
SAU802711	MGE100390	44%	97.6%	98.9%
SAU802711	MPN100285	41%	97.9%	99.2%
SAU802711	NGO100779	47%	98.2%	97.8%
SAU802711	NME200069	47%	98.2%	98.2%
SAU802711	PMU101485	51%	99.2%	99.0%
SAU802711	PRT103989	51%	99.2%	98.9%
SAU802711	PAE205560	50%	98.1%	97.3%
SAU802711	PPU103677	50%	97.8%	98.2%
SAU802711	PSY103430	49%	57.1%	97.0%
SAU802711	SPA103411	50%	98.9%	99.7%
SAU802711	STY103850	51%	98.9%	98.7%
SAU802711	SAU802711	100%	100%	100%
SAU802711	SEP201293	93%	99.7%	99.7%
SAU802711	SHA101596	94%	100%	100%
SAU802711	SMU101356	63%	98.2%	97.8%
SAU802711	SPN400124	63%	99.5%	98.0%
SAU802711	SPY201670	63%	99.2%	98.7%
SAU802711	TPA100043	42%	98.2%	99.0%
SAU802711	UUR100037	46%	98.9%	99.7%
SAU802711	VCH102736	49%	98.4%	97.8%
SAU802711	YPS000011	50%	99.0%	98.9%
SAU802713	ABA100989	26%	83.5%	73.7%
SAU802713	BAN108182	50%	89.6%	90.4%
SAU802713	BAN113266	51%	91.3%	89.1%
SAU802713	BFR101294	30%	64.3%	55.8%
SAU802713	BPT105773	40%	35.7%	34.1%
SAU802713	BBU100440	23%	82.6%	82.4%
SAU802713	BMA108699	29%	69.6%	51.0%
SAU802713	CJU100890	23%	95.7%	99.1%
SAU802713	CPN200910	34%	72.2%	59.0%
SAU802713	CTR200162	26%	71.3%	68.9%
SAU802713	CAC102336	38%	91.3%	89.9%
SAU802713	CBO103162	37%	94.8%	99.1%
SAU802713	CDF103808	40%	86.1%	87.7%
SAU802713	CDP101660	29%	54.8%	53.8%
SAU802713	EBC100049	28%	70.4%	89.0%
SAU802713	EFA200678	44%	96.5%	94.9%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802713	EFM102258	42%	60.9%	97.3%
SAU802713	ECO103625	26%	83.5%	80.7%
SAU802713	HIN100980	28%	69.6%	67.2%
SAU802713	HPY101427	27%	94.8%	80.7%
SAU802713	KPN302213	32%	55.7%	54.6%
SAU802713	LPN100279	32%	96.5%	96.5%
SAU802713	LMO102928	52%	98.3%	95.8%
SAU802713	MCA103188	32%	73.0%	62.0%
SAU802713	MBV103340	24%	88.7%	81.6%
SAU802713	MLP101604	21%	89.6%	92.5%
SAU802713	MTU203868	24%	88.7%	81.6%
SAU802713	MGE100474	28%	86.1%	89.8%
SAU802713	NGO101432	28%	88.7%	85.1%
SAU802713	NME200510	28%	88.7%	85.1%
SAU802713	PMU101163	29%	64.3%	56.9%
SAU802713	PRT102997	33%	55.7%	54.6%
SAU802713	PAE205564	31%	70.4%	60.7%
SAU802713	PPU102196	38%	42.6%	30.3%
SAU802713	PSY107592	33%	64.3%	43.6%
SAU802713	STY104781	27%	83.5%	80.7%
SAU802713	STM104793	27%	83.5%	80.7%
SAU802713	SAU802713	100%	100%	100%
SAU802713	SEP201290	83%	100%	100%
SAU802713	SHA100141	83%	100%	100%
SAU802713	SMU100665	44%	97.4%	93.3%
SAU802713	SPN401851	45%	97.4%	91.1%
SAU802713	SPY200178	46%	97.4%	93.3%
SAU802713	UUR100610	31%	93.0%	92.9%
SAU802713	VCH100006	33%	76.5%	74.6%
SAU802713	YPS003466	33%	56.5%	55.5%
SAU802714	ABA100986	62%	95.6%	97.7%
SAU802714	BAN102648	88%	97.8%	100%
SAU802714	BAN102568	88%	97.8%	100%
SAU802714	BFR106080	62%	95.6%	91.5%
SAU802714	BPT100632	53%	95.6%	97.7%
SAU802714	BBU100439	55%	95.6%	84.3%
SAU802714	BCE105407	55%	95.6%	97.7%
SAU802714	BMA109034	55%	95.6%	97.7%
SAU802714	CJU100891	60%	95.6%	97.7%
SAU802714	CPN200909	64%	93.3%	93.3%
SAU802714	CTR200163	61%	93.3%	93.3%
SAU802714	CAC101976	70%	91.1%	93.2%
SAU802714	CBO101345	63%	91.1%	70.7%
SAU802714	CDF104319	70%	97.8%	97.8%
SAU802714	CDP101663	58%	95.6%	86%
SAU802714	EBC100048	62%	95.6%	93.5%
SAU802714	EFA202663	86%	97.8%	100%
SAU802714	ECO103624	62%	95.6%	93.5%
SAU802714	HIN100979	70%	97.8%	100%
SAU802714	HPY101426	60%	95.6%	97.7%
SAU802714	KPN204278	62%	95.6%	93.5%
SAU802714	LPN103600	61%	97.8%	100%
SAU802714	LMO100377	84%	97.8%	100%
SAU802714	MCA103596	60%	95.6%	97.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
SAU802714	MBV102731	59%	93.3%	91.3%
SAU802714	MLP101605	58%	95.6%	91.5%
SAU802714	MTU203869	60%	95.6%	91.5%
SAU802714	MGE100475	58%	95.6%	89.6%
SAU802714	MPN100160	58%	95.6%	89.6%
SAU802714	NGO103743	55%	95.6%	97.7%
SAU802714	NME200511	55%	95.6%	97.7%
SAU802714	PMU101162	70%	97.8%	100%
SAU802714	PRT102996	60%	95.6%	91.5%
SAU802714	PAE205565	65%	95.6%	97.7%
SAU802714	PPU102199	62%	95.6%	97.7%
SAU802714	SPA101308	62%	95.6%	93.5%
SAU802714	STY104683	62%	95.6%	93.5%
SAU802714	STM104752	62%	95.6%	93.5%
SAU802714	SAU802714	100%	100%	100%
SAU802714	SEP201288	100%	100%	100%
SAU802714	SHA100140	100%	100%	100%
SAU802714	SMU102293	72%	97.8%	100%
SAU802714	SPN401805	72%	97.8%	100%
SAU802714	SPY200181	75%	97.8%	100%
SAU802714	TPA100941	55%	95.6%	84.3%
SAU802714	UUR100611	72%	95.6%	89.6%
SAU802714	VCH100007	63%	97.8%	97.8%
SAU802714	YPS003462	60%	95.6%	93.5%
STM100137	BPT103857	29%	85.4%	59.3%
STM100137	BFU113310	31%	82.2%	80.5%
STM100137	BMA106841	30%	83.6%	48.9%
STM100137	PAE111701	33%	15.5%	64.5%
STM100137	PPU102760	32%	23.2%	28.5%
STM100137	SPA106841	87%	7.0%	70.9%
STM100137	STM100137	100%	100%	100%
STM100137	SAU501115	27%	19.6%	25.6%
STM100227	BCE105792	22%	31.0%	52.5%
STM100227	BCE101253	29%	25.5%	38.4%
STM100227	BFU102165	29%	15.8%	32.0%
STM100227	KPN109637	48%	15.6%	92.1%
STM100227	STM100227	100%	100%	100%
STM100227	SAU502668	32%	7.2%	20.1%
STM100229	BCE113297	41%	41.4%	100%
STM100229	BMA101920	35%	95.7%	91.3%
STM100229	CDP102420	32%	12.3%	94.7%
STM100229	KPN112130	68%	29.7%	89.1%
STM100229	MAV107220	28%	93.7%	93.8%
STM100229	PAE111649	34%	78.5%	92.8%
STM100229	SPA106013	100%	13.6%	74.4%
STM100229	STM100229	100%	100%	100%
STM100229	SMU101194	24%	17.2%	21.3%
STM100274	ABA101013	37%	89.8%	93.7%
STM100274	ABA100365	41%	89.8%	93.7%
STM100274	BPT100083	36%	96.5%	100%
STM100274	BCE104632	39%	81.9%	100%
STM100274	BFU102105	41%	92.7%	96.1%
STM100274	BMA108617	42%	90.5%	94.0%
STM100274	EBC100961	77%	99.7%	98.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
STM100274	ECO101491	84%	98.7%	96.9%
STM100274	KPN306347	56%	96.5%	100%
STM100274	LPN103390	29%	69.5%	95.5%
STM100274	MCA100493	34%	96.5%	100%
STM100274	MLP100143	35%	15.2%	8.4%
STM100274	PRT101607	55%	94.0%	100%
STM100274	PPU106304	37%	94.3%	98.0%
STM100274	PSY103291	29%	81.3%	90.3%
STM100274	SPA103363	96%	98.7%	96.9%
STM100274	STY104266	99%	100%	100%
STM100274	STM100274	100%	100%	100%
STM100541	MAV101179	24%	26.4%	27.1%
STM100541	STM100541	100%	100%	100%
STM100580	BPT103484	40%	96.2%	68.4%
STM100580	BCE114868	44%	86.6%	96.9%
STM100580	BMA108364	24%	49.4%	48.6%
STM100580	PPU111837	30%	91.7%	71.4%
STM100580	SPA107052	72%	11.8%	86.0%
STM100580	STM100580	100%	100%	100%
STM100637	BMA101649	23%	82.3%	55.3%
STM100637	EBC104360	25%	17.3%	15.9%
STM100637	ECO103620	25%	14.5%	13.2%
STM100637	KPN301149	25%	17.3%	30.6%
STM100637	PRT102211	27%	11.9%	10.9%
STM100637	STY103968	25%	17.3%	15.9%
STM100637	STM101609	40%	97.6%	95.8%
STM100637	STM100637	100%	100%	100%
STM100638	BCE104424	35%	13.2%	39.6%
STM100638	STM100638	100%	100%	100%
STM100693	STM100290	28%	79.6%	80.3%
STM100693	STM100693	100%	100%	100%
STM100723	ABA104878	49%	99.2%	99.0%
STM100723	BAN106141	34%	43.8%	99.7%
STM100723	BAN102570	46%	43.8%	96.9%
STM100723	BFR101415	47%	42.9%	93.2%
STM100723	BPT101834	29%	44.5%	42.5%
STM100723	BBU100588	35%	42.6%	91.5%
STM100723	BCE113410	44%	36.6%	95.4%
STM100723	BFU103363	44%	44.3%	93.9%
STM100723	BMA102976	32%	43.7%	41.4%
STM100723	CJU100638	49%	45.4%	64.9%
STM100723	CAC102832	45%	44.1%	97.0%
STM100723	CBO102063	55%	22.4%	90.4%
STM100723	CDF100616	23%	44.4%	97.6%
STM100723	CDF100432	24%	43.8%	96.0%
STM100723	CDP101294	43%	59.5%	91.4%
STM100723	EBC104962	91%	99.9%	100%
STM100723	EFA202248	44%	42.6%	93.6%
STM100723	EFM200028	38%	26.9%	93.7%
STM100723	ECO102255	96%	99.9%	100%
STM100723	HIN101176	68%	99.6%	100%
STM100723	HPY200837	50%	30.5%	6.7%
STM100723	KPN305976	95%	99.3%	100%
STM100723	LPN102073	27%	26.3%	41.0%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
STM100723	LMO100950	47%	42.7%	93.8%
STM100723	MCA101508	64%	23.8%	1.4%
STM100723	MAV101929	36%	99.3%	98.6%
STM100723	MBV102834	36%	99.2%	98.8%
STM100723	MTU200407	36%	99.2%	98.8%
STM100723	MGE100305	35%	44.7%	97.5%
STM100723	MPN100413	36%	44.0%	97.2%
STM100723	NGO100804	70%	17.5%	8.2%
STM100723	NME200777	70%	17.5%	8.2%
STM100723	PMU100705	69%	99.6%	100%
STM100723	PRT100628	81%	99.3%	100%
STM100723	PAE200834	55%	98.9%	98.9%
STM100723	PPU103956	50%	98.6%	100%
STM100723	PSY102379	52%	97.5%	99.4%
STM100723	SPA102048	91%	70.3%	93.3%
STM100723	STY100983	99%	100%	100%
STM100723	STM100723	100%	100%	100%
STM100723	SAU800588	42%	43.0%	94.8%
STM100723	SEP200137	44%	43.0%	94.8%
STM100723	SHA101700	45%	43.0%	94.8%
STM100723	SMU100210	45%	42.6%	92.4%
STM100723	SPN401007	48%	43.1%	95.1%
STM100723	SPY200858	44%	43.3%	94.0%
STM100723	TPA100093	41%	43.3%	95.5%
STM100723	UUR100064	24%	35.4%	82.9%
STM100723	VCH101078	73%	100%	100%
STM100723	YPS000496	86%	99.6%	99.2%
STM100724	BAN104006	29%	73.1%	91.0%
STM100724	BAN106594	29%	97.8%	96.6%
STM100724	BFR103701	31%	95.7%	97.4%
STM100724	BPT103061	21%	19.2%	22.9%
STM100724	BBU100842	29%	95.7%	96.3%
STM100724	BMA107628	29%	77.9%	72.5%
STM100724	CTR100660	29%	20.8%	36.2%
STM100724	CBO103750	28%	98.4%	98.8%
STM100724	CDF101574	35%	76.5%	87.3%
STM100724	CDF101198	35%	98.0%	97.0%
STM100724	CDP101707	39%	11.5%	12.1%
STM100724	EBC103307	30%	96.0%	98.3%
STM100724	EFA202432	26%	80.6%	87.0%
STM100724	EFM200181	50%	5.1%	15.1%
STM100724	ECO102256	91%	100%	98.6%
STM100724	HIN100573	28%	97.2%	97.8%
STM100724	HPY100684	24%	35.2%	38.1%
STM100724	MCA100770	21%	72.7%	73.0%
STM100724	PMU101104	23%	34.0%	34.4%
STM100724	PRT100826	29%	96.4%	96.4%
STM100724	SPA102153	96%	97.8%	100%
STM100724	STY100984	100%	100%	100%
STM100724	STM100724	100%	100%	100%
STM100724	SAU801171	29%	97.6%	97.3%
STM100724	SEP202232	28%	97.4%	96.5%
STM100724	SHA102381	30%	97.6%	98.1%
STM100724	SMU100142	21%	76.7%	79.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
STM100724	SPN401956	28%	98.2%	98.2%
STM100724	SPY201191	27%	98.2%	99.4%
STM100724	VCH100864	23%	43.1%	41.8%
STM100724	YPS002032	19%	20.6%	39.7%
STM100866	BPT101006	33%	97.9%	91.7%
STM100866	BCE100250	33%	52.9%	98.0%
STM100866	BFU108046	30%	97.2%	99.7%
STM100866	BFU106928	32%	95.5%	94.2%
STM100866	BFU101670	31%	95.8%	97.1%
STM100866	BFU102611	33%	97.2%	94.9%
STM100866	BFU110913	33%	95.2%	95.9%
STM100866	BFU114233	33%	96.2%	97.3%
STM100866	BMA106862	28%	95.8%	92.0%
STM100866	CDP100121	25%	97.6%	96.4%
STM100866	EBC102104	73%	98.6%	98.3%
STM100866	EFA200698	55%	97.6%	95.6%
STM100866	ECO100606	63%	99.7%	94.5%
STM100866	HIN100022	61%	100%	99.7%
STM100866	KPN201811	89%	100%	100%
STM100866	MCA100880	23%	95.5%	97.0%
STM100866	MAV100316	30%	97.9%	95.2%
STM100866	MBV101161	31%	88.2%	86.8%
STM100866	MTU202461	31%	88.2%	86.8%
STM100866	PRT106096	26%	96.9%	97.5%
STM100866	PAE200882	30%	97.6%	97.5%
STM100866	PPU100881	28%	30.1%	11.6%
STM100866	SPA101729	96%	92.7%	100%
STM100866	STY101151	99%	100%	100%
STM100866	STM100866	100%	100%	100%
STM100866	SMU100150	56%	99.0%	95.7%
STM100866	SPY200907	57%	99.0%	97.3%
STM100866	VCH100784	65%	98.6%	96.6%
STM100866	YPS002471	30%	97.9%	96.1%
STM101115	BAN112350	30%	33.4%	40.1%
STM101115	BCE100786	33%	27.5%	28.5%
STM101115	BFU102061	27%	36.4%	39.9%
STM101115	BMA109995	30%	35.2%	35.3%
STM101115	CAC101453	33%	88.5%	81.3%
STM101115	CBO101891	30%	31.1%	33.8%
STM101115	CDF103042	31%	25.1%	48.3%
STM101115	CDP100635	25%	76.3%	82.6%
STM101115	EBC103957	84%	97.6%	100%
STM101115	EFA201896	22%	30.5%	33.6%
STM101115	ECO103737	81%	99.4%	98.8%
STM101115	HIN100626	30%	93.8%	98.4%
STM101115	KPN303520	81%	97.0%	99.4%
STM101115	LMO101007	29%	29.0%	32.4%
STM101115	MAV102145	25%	39.9%	47.3%
STM101115	MBV102643	28%	39.9%	47.0%
STM101115	MLP101539	23%	83.7%	92.8%
STM101115	MTU200182	28%	39.9%	40.6%
STM101115	MPN100368	48%	10.4%	13.1%
STM101115	PMU101631	28%	93.5%	97.5%
STM101115	PRT104544	48%	95.9%	97.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
STM101115	PAE203299	28%	28.4%	30.4%
STM101115	PPU108432	30%	28.4%	30.6%
STM101115	SPA101172	97%	100%	100%
STM101115	STY102009	99%	100%	100%
STM101115	STM101115	100%	100%	100%
STM101115	SAU801303	30%	44.4%	48.0%
STM101115	SEP201929	29%	35.2%	39.3%
STM101115	SHA102823	29%	29.9%	31.9%
STM101115	VCH100134	37%	93.8%	92.9%
STM101115	YPS001338	57%	97.6%	97.9%
STM101116	BAN105201	25%	87.6%	89.6%
STM101116	BAN104169	29%	90.2%	89.0%
STM101116	BBU100068	31%	97.7%	96.2%
STM101116	BCE113428	43%	30.5%	90%
STM101116	BFU104191	37%	99.2%	97.1%
STM101116	BMA100853	37%	99.2%	96.0%
STM101116	CPN200343	24%	89.5%	88.8%
STM101116	CTR200373	21%	89.8%	88.6%
STM101116	CAC101546	26%	90.2%	90.2%
STM101116	CAC100913	27%	88.3%	86.9%
STM101116	CAC101334	27%	90.2%	90%
STM101116	CBO101559	24%	89.8%	90.3%
STM101116	CDF102915	26%	89.5%	87.9%
STM101116	EBC103959	89%	99.6%	97.8%
STM101116	EFA202119	26%	90.6%	91.0%
STM101116	EFM200109	29%	90.2%	91.0%
STM101116	ECO103738	90%	57.5%	89.5%
STM101116	HIN100576	42%	98.9%	97.1%
STM101116	KPN303521	81%	99.6%	99.6%
STM101116	LMO102621	27%	90.6%	91.3%
STM101116	MAV103247	25%	98.9%	98.5%
STM101116	MBV102452	26%	87.2%	87.2%
STM101116	MLP100060	26%	96.6%	92.9%
STM101116	MTU203758	26%	87.2%	87.2%
STM101116	MPN100414	27%	80.5%	79.7%
STM101116	NGO100507	38%	34.2%	80.7%
STM101116	PMU101629	40%	98.9%	97.1%
STM101116	PRT105543	62%	99.2%	99.2%
STM101116	SPA101171	99%	75.2%	100%
STM101116	STY102007	100%	100%	100%
STM101116	STM101116	100%	100%	100%
STM101116	SAU801331	27%	98.5%	98.5%
STM101116	SEP200102	28%	90.6%	90.1%
STM101116	SHA100656	26%	98.1%	95.6%
STM101116	SMU100748	27%	98.5%	100%
STM101116	SPN400263	30%	98.9%	98.9%
STM101116	SPY201336	28%	98.9%	98.9%
STM101116	TPA100287	25%	89.1%	88.4%
STM101116	UUR100174	26%	88.7%	88.0%
STM101116	VCH100133	49%	97.4%	94.9%
STM101116	YPS001335	73%	99.6%	98.5%
STM101278	EBC107120	29%	17.1%	60.9%
STM101278	NME105091	31%	15.2%	17.7%
STM101278	PSY106217	25%	53.1%	52.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
STM101278	STM101278	100%	100%	100%
STM101278	SEP200437	28%	24.6%	34.2%
STM101278	SEP200202	28%	24.6%	34.2%
STM101278	SEP200828	28%	24.6%	34.2%
STM101278	SEP204358	36%	12.4%	36.5%
STM101278	SEP200771	28%	24.6%	34.2%
STM101278	SEP201864	28%	24.6%	34.2%
STM101278	SEP200165	28%	24.6%	34.2%
STM101278	SEP201913	28%	24.6%	34.2%
STM101278	SEP200187	28%	24.6%	34.2%
STM101278	SEP200347	28%	24.6%	34.2%
STM101278	SEP203770	28%	24.6%	34.2%
STM101278	SEP200222	28%	24.6%	34.2%
STM101923	BFR104413	56%	97.8%	95.5%
STM101923	BPT102042	44%	96.9%	95.0%
STM101923	BCE112542	59%	97.8%	97.8%
STM101923	BFU104304	58%	96.9%	93.0%
STM101923	BMA105070	57%	97.8%	97.4%
STM101923	CAC101675	30%	89.3%	84.0%
STM101923	CBO102946	31%	87.5%	83.9%
STM101923	CDF104256	28%	90.2%	89.3%
STM101923	CDP100150	30%	98.7%	97.9%
STM101923	EBC101616	89%	38.7%	100%
STM101923	EFA202385	30%	91.9%	88.7%
STM101923	ECO101796	90%	100%	92.5%
STM101923	KPN301541	79%	99.3%	99.6%
STM101923	MAV103783	30%	88.8%	74.1%
STM101923	MBV105656	29%	88.2%	77.6%
STM101923	MTU202299	29%	88.2%	75.6%
STM101923	PAE200245	30%	89.7%	82.8%
STM101923	SPA100492	98%	98.9%	100%
STM101923	STM101923	100%	100%	100%
STM101923	VCH101573	28%	88.6%	84.9%
STM101923	YPS000541	69%	98.9%	99.3%
STM101955	SPA104151	96%	100%	100%
STM101955	STM101955	100%	100%	100%
STM102011	STM102011	100%	100%	100%
STM102089	ABA104944	29%	76.3%	81.9%
STM102089	BAN113702	44%	45.9%	72.6%
STM102089	BAN111016	34%	98.2%	100%
STM102089	BAN102075	36%	93.0%	90.5%
STM102089	BAN106548	36%	100%	99.4%
STM102089	BAN111025	34%	100%	100%
STM102089	BFR100859	25%	46.2%	35.5%
STM102089	BFR102551	26%	49.8%	38.2%
STM102089	BPT101117	35%	98.2%	91.8%
STM102089	BCE102679	33%	98.8%	92.7%
STM102089	BFU105518	35%	86.6%	79.7%
STM102089	BMA107904	35%	98.8%	100%
STM102089	CJU100150	33%	92.7%	93.1%
STM102089	CPN200938	28%	20.4%	18.7%
STM102089	CAC101752	32%	98.8%	100%
STM102089	CBO102636	31%	98.8%	99.7%
STM102089	CDF101204	30%	98.8%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
STM102089	CDP101688	31%	86.0%	98.0%
STM102089	EBC102210	89%	100%	100%
STM102089	EFA202347	35%	98.8%	100%
STM102089	ECO100757	92%	100%	100%
STM102089	HIN101641	60%	99.4%	96.7%
STM102089	HPY100755	28%	98.8%	99.7%
STM102089	KPN303579	87%	100%	100%
STM102089	LMO102857	33%	98.8%	99.1%
STM102089	MCA103672	44%	99.1%	89.5%
STM102089	MAV105594	35%	95.1%	87.4%
STM102089	MBV102851	33%	92.4%	83.4%
STM102089	MTU203069	33%	92.4%	85.5%
STM102089	PMU100625	61%	98.8%	96.1%
STM102089	PRT104379	72%	99.1%	99.4%
STM102089	PAE201504	35%	99.4%	99.1%
STM102089	PPU106301	36%	93.3%	92.2%
STM102089	PSY105427	35%	98.2%	99.7%
STM102089	SPA102732	99%	100%	100%
STM102089	STY102330	100%	100%	100%
STM102089	STM102089	100%	100%	100%
STM102089	SAU802268	33%	100%	100%
STM102089	SEP200319	32%	100%	100%
STM102089	SHA101565	31%	100%	100%
STM102089	SPN400676	25%	48.6%	47.9%
STM102089	VCH101005	64%	100%	98.5%
STM102089	YPS002149	76%	99.1%	99.4%
STM102090	BAN104975	42%	84.7%	85.8%
STM102090	BFR102256	23%	81.2%	38.5%
STM102090	BPT101121	52%	91.8%	90.2%
STM102090	EBC102209	91%	100%	100%
STM102090	ECO100758	95%	100%	100%
STM102090	KPN303581	92%	100%	100%
STM102090	LMO101377	38%	87.1%	91.4%
STM102090	MCA101697	58%	95.9%	86.2%
STM102090	MBV100621	31%	81.8%	76.8%
STM102090	MLP100125	33%	81.2%	76.2%
STM102090	MTU200973	31%	81.8%	76.8%
STM102090	PAE203912	58%	97.1%	89.2%
STM102090	PAE203027	58%	95.9%	91.1%
STM102090	PPU101063	57%	97.6%	96.5%
STM102090	PSY109125	54%	99.4%	94.4%
STM102090	SPA102733	99%	100%	100%
STM102090	STY102331	100%	100%	100%
STM102090	STM102090	100%	100%	100%
STM102090	SAU802275	45%	85.3%	87.5%
STM102090	SEP200340	42%	85.9%	85.2%
STM102090	SHA101559	46%	84.1%	84.8%
STM102090	SMU101232	25%	56.5%	21.3%
STM102090	SPN401756	29%	51.8%	19.4%
STM102090	VCH101006	63%	98.8%	98.8%
STM102366	STM102366	100%	100%	100%
STM102401	BPT105648	41%	100%	42.0%
STM102401	BCE107576	40%	99.4%	73.4%
STM102401	BFU113002	41%	45.3%	33.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
STM102401	BMA104672	37%	99.4%	47.0%
STM102401	MAV108057	34%	99.4%	76.8%
STM102401	MBV105368	35%	99.4%	80.3%
STM102401	MTU409357	35%	99.4%	80.3%
STM102401	PAE109984	40%	99.4%	89.1%
STM102401	PSY100104	42%	95.0%	95.6%
STM102401	STM102401	100%	100%	100%
STM102419	BPT105323	33%	92.8%	49.0%
STM102419	PAE111918	43%	64.0%	51.8%
STM102419	PSY103395	35%	91.9%	54.3%
STM102419	SPA106234	100%	100%	82.2%
STM102419	STM102419	100%	100%	100%
STM102422	CDP102587	30%	73.9%	35.2%
STM102422	EBC105759	91%	48.9%	100%
STM102422	KPN206188	95%	48.9%	100%
STM102422	STM102422	100%	100%	100%
STM102449	BFU104448	49%	99.2%	67.8%
STM102449	MBV100454	32%	99.2%	80%
STM102449	MTU411274	32%	99.2%	80%
STM102449	PRT105025	61%	48%	88.6%
STM102449	PAE111567	48%	23.2%	96.7%
STM102449	STM102449	100%	100%	100%
STM102449	SPY103286	52%	38.4%	98.0%
STM102672	ABA105833	40%	96.4%	99.4%
STM102672	BAN101367	20%	65.6%	68.2%
STM102672	BPT101286	48%	97.5%	99.2%
STM102672	BBU100809	25%	96.6%	97.5%
STM102672	BCE109401	52%	97.1%	99.6%
STM102672	BFU100360	52%	97.1%	99.6%
STM102672	BMA106132	50%	98.1%	81.1%
STM102672	CJU100740	31%	86.3%	92.5%
STM102672	CPN200015	23%	82.6%	78.1%
STM102672	CTR200901	22%	88.4%	83.6%
STM102672	CAC103368	27%	82.8%	82.5%
STM102672	CBO100146	25%	84.4%	93.0%
STM102672	CDF100314	28%	23.1%	87.4%
STM102672	CDF100311	26%	70.2%	91.0%
STM102672	CDF103058	27%	95.6%	95.6%
STM102672	CDP101613	25%	77.9%	37.2%
STM102672	EBC101202	91%	97.5%	100%
STM102672	EFA201075	21%	72.5%	75.7%
STM102672	EFM201627	23%	43.9%	42.0%
STM102672	ECO101042	94%	97.3%	99.8%
STM102672	HIN100943	39%	93.5%	98.4%
STM102672	HPY100871	28%	83.8%	98.0%
STM102672	KPN302527	90%	100%	100%
STM102672	LPN102528	45%	87.0%	98.7%
STM102672	LMO100585	23%	36.6%	33.5%
STM102672	MCA103523	43%	95.4%	97.7%
STM102672	MBV102833	27%	79.8%	37.1%
STM102672	MLP101595	27%	91.6%	40.0%
STM102672	MTU203855	27%	80.7%	36.7%
STM102672	NGO101881	64%	96.9%	99.4%
STM102672	NME202045	63%	96.9%	99.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
STM102672	PMU101660	40%	93.5%	98.4%
STM102672	PRT101541	76%	97.1%	99.6%
STM102672	PAE204560	76%	97.1%	99.4%
STM102672	PPU112503	71%	97.1%	99.4%
STM102672	PSY102688	74%	93.5%	99.4%
STM102672	SPA100422	94%	100%	100%
STM102672	STY102506	99%	94.8%	100%
STM102672	STM102672	100%	100%	100%
STM102672	SAU801754	20%	40.8%	38.9%
STM102672	SEP202115	20%	40.3%	38.5%
STM102672	SHA101207	19%	78.4%	75.0%
STM102672	SMU100383	21%	40.8%	38.2%
STM102672	SPN401382	24%	26.0%	25.2%
STM102672	TPA100512	25%	89.5%	88.4%
STM102672	VCH100667	41%	97.9%	99.0%
STM102672	YPS003371	85%	97.3%	99.8%
STM102789	ABA101658	46%	92.6%	91.1%
STM102789	BAN113740	23%	69.7%	78.7%
STM102789	BAN102304	24%	87.7%	91.5%
STM102789	BFR10945	29%	87.7%	82.8%
STM102789	BPT100037	45%	96.7%	89.4%
STM102789	BCE110334	52%	91.0%	62.7%
STM102789	BFU105764	51%	91.0%	48.1%
STM102789	BMA107802	48%	91.0%	61.3%
STM102789	CJU100229	41%	86.1%	89.0%
STM102789	CAC100848	21%	89.3%	47.0%
STM102789	CBO101544	27%	92.6%	48.7%
STM102789	CDF103965	27%	88.5%	45.2%
STM102789	EBC104206	81%	100%	100%
STM102789	EFA200393	24%	87.7%	80.5%
STM102789	EFM201127	27%	83.6%	77.9%
STM102789	ECO103936	86%	99.2%	99.2%
STM102789	HIN100318	45%	93.4%	96.6%
STM102789	HPY100691	41%	88.5%	84.4%
STM102789	KPN306685	80%	28.7%	97.2%
STM102789	KPN306067	78%	34.4%	97.7%
STM102789	KPN301864	83%	99.2%	99.2%
STM102789	LMO102033	29%	86.1%	80.2%
STM102789	NGO101285	40%	88.5%	85.0%
STM102789	NME201605	40%	87.7%	84.3%
STM102789	PMU101864	50%	93.4%	96.6%
STM102789	PRT101484	64%	99.2%	98.4%
STM102789	PAE203601	50%	91.8%	91.1%
STM102789	PPU101143	50%	91.8%	92.6%
STM102789	PSY104412	45%	91.8%	92.6%
STM102789	SPA103524	99%	100%	100%
STM102789	STY101940	100%	100%	100%
STM102789	STM102789	100%	100%	100%
STM102789	SAU801569	28%	90.2%	96.5%
STM102789	SEP201025	31%	81.1%	83.9%
STM102789	SHA101649	34%	57.4%	97.2%
STM102789	SMU101129	38%	77.0%	70.1%
STM102789	SPN400870	34%	82.0%	77.9%
STM102789	SPY200341	31%	91.0%	85.9%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
STM102789	VCH103435	58%	95.9%	99.2%
STM102789	YPS002785	67%	98.4%	97.6%
STM102835	BAN100006	22%	40.4%	67.4%
STM102835	BFR106009	25%	50.8%	36.6%
STM102835	BPT100671	23%	68.2%	40.9%
STM102835	BCE102211	26%	1.3%	30.4%
STM102835	BCE104738	24%	53.1%	59.1%
STM102835	BCE103017	25%	40.6%	90.6%
STM102835	BCE110445	26%	35.6%	94.0%
STM102835	BCE103623	26%	1.6%	96.7%
STM102835	BCE110366	23%	13.5%	38.0%
STM102835	BCE101250	24%	61.2%	55.7%
STM102835	BCE100403	25%	3.8%	94.4%
STM102835	BFU113446	21%	12.9%	55.0%
STM102835	BFU106257	21%	16.8%	73.7%
STM102835	BFU112017	23%	53.6%	73.3%
STM102835	BFU104375	23%	53.6%	42.8%
STM102835	BFU106700	23%	46.7%	39.2%
STM102835	BFU112565	21%	69.6%	66.3%
STM102835	BFU109807	23%	53.3%	69.1%
STM102835	BFU108657	22%	54.3%	87.1%
STM102835	BMA108282	26%	58.6%	88.4%
STM102835	CJU101583	22%	16.3%	57.3%
STM102835	CJU100590	22%	61.9%	1.7%
STM102835	CTR200684	18%	40.1%	78.3%
STM102835	CBO102757	30%	3.9%	10.6%
STM102835	CDF101661	31%	8.4%	12.5%
STM102835	CDP101991	22%	13.8%	24.4%
STM102835	EFA201471	23%	63.7%	34.5%
STM102835	EFM200844	23%	57.8%	25.0%
STM102835	ECO101376	47%	12.6%	66.5%
STM102835	HPY200552	22%	40.9%	61.1%
STM102835	HPY200273	20%	48.7%	23.6%
STM102835	HPY200815	19%	41.3%	64.1%
STM102835	HPY200852	21%	1.4%	6.3%
STM102835	KPN206267	23%	9.4%	28.1%
STM102835	MAV104123	30%	5.6%	60.7%
STM102835	MBV102102	23%	63.2%	14.2%
STM102835	MTU200354	21%	56.0%	88.8%
STM102835	MTU200303	23%	17.8%	78.1%
STM102835	NME200634	21%	47.9%	41.9%
STM102835	SPA103181	85%	35.0%	97.7%
STM102835	STM102835	100%	100%	100%
STM102835	SAU800561	24%	12.7%	16.7%
STM102835	SAU800562	22%	30.5%	2.5%
STM102835	SAU800563	26%	10.9%	15.7%
STM102835	SAU800811	21%	12.4%	34.5%
STM102835	SAU802630	27%	8.3%	16.1%
STM102835	SEP100151	29%	7.2%	19.9%
STM102835	SEP100719	25%	7.7%	2.1%
STM102835	SHA100562	19%	79.5%	4.8%
STM102835	SMU101698	19%	49.7%	91.5%
STM102835	SPY201332	21%	7.1%	32.8%
STM102835	VCH101430	20%	22.5%	81.9%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
STM103180	BFR14231	25%	13.8%	43.0%
STM103180	BCE105486	36%	92.0%	95.5%
STM103180	EBC101869	50%	79.4%	98.6%
STM103180	ECO102296	58%	65.4%	100%
STM103180	PRT104898	38%	90.4%	98.7%
STM103180	PRT104430	46%	93.8%	93.3%
STM103180	PRT100691	48%	96.8%	97.2%
STM103180	SPA103176	90%	93.9%	100%
STM103180	STY103516	53%	98.9%	97.2%
STM103180	STM103180	100%	100%	100%
STM103180	YPS002772	44%	92.5%	97.5%
STM103235	CAC102031	25%	13.4%	43.5%
STM103235	CBO103445	29%	9.5%	35.5%
STM103235	ECO103932	20%	51.5%	84.6%
STM103235	KPN301199	31%	12.1%	13.0%
STM103235	SPA103638	95%	76.5%	100%
STM103235	STM103235	100%	100%	100%
STM103235	YPS000110	32%	12.1%	13.0%
STM103247	BCE107517	29%	82.1%	70.2%
STM103247	BMA103289	32%	58.0%	58.2%
STM103247	KPN207172	50%	10.1%	58.3%
STM103247	PPU107587	30%	79.8%	76%
STM103247	PSY106811	32%	81.8%	84.1%
STM103247	SPA106549	94%	14.6%	59.1%
STM103247	STM103247	100%	100%	100%
STM103274	BFU113111	30%	27.2%	15.5%
STM103274	STM103274	100%	100%	100%
STM103418	EBC106113	76%	98.4%	52.1%
STM103418	STM103418	100%	100%	100%
STM103506	KPN200136	32%	27.7%	23.2%
STM103506	SPA105363	92%	11.8%	65.1%
STM103506	STM103506	100%	100%	100%
STM103802	BMA103619	25%	42.7%	73.4%
STM103802	BMA106999	27%	87.2%	94.5%
STM103802	HPY201193	24%	11.9%	69.1%
STM103802	STM103802	100%	100%	100%
STM103805	ABA102812	33%	16.9%	22.1%
STM103805	ABA105767	23%	62.4%	49.5%
STM103805	ABA106133	25%	63.4%	49.3%
STM103805	BFR100630	24%	29.9%	36.1%
STM103805	BCE104450	37%	39.2%	94.1%
STM103805	BCE111308	33%	80.9%	94.6%
STM103805	BFU107929	43%	79.0%	88.5%
STM103805	BFU100791	45%	78.7%	82.5%
STM103805	BFU102584	45%	80.4%	90.2%
STM103805	BMA104805	46%	71.3%	78.0%
STM103805	EBC102287	37%	80.2%	67.4%
STM103805	ECO200602	33%	74.3%	84.2%
STM103805	ECO202018	32%	77.5%	76.6%
STM103805	ECO200236	32%	78.7%	78.0%
STM103805	KPN305296	25%	69.4%	61.5%
STM103805	MBV100192	36%	12.2%	27.2%
STM103805	MTU202980	35%	11.2%	20.3%
STM103805	PRT100729	28%	77.0%	77.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
STM103805	PRT101866	27%	95.9%	91.5%
STM103805	PAE202683	38%	77.6%	77.4%
STM103805	PAE200091	37%	83.8%	94.2%
STM103805	PAE200095	39%	81.6%	96.0%
STM103805	PPU110472	34%	80.9%	95.3%
STM103805	PSY102082	32%	83.8%	90%
STM103805	SPA102886	79%	97.7%	100%
STM103805	STY104093	99%	100%	100%
STM103805	STM103805	100%	100%	100%
STM103805	VCH102859	27%	82.7%	60.0%
STM103805	VCH101395	30%	79.8%	50.5%
STM103805	VCH102754	31%	78.5%	83.4%
STM103805	YPS002256	38%	85.7%	72.9%
STM103815	STM103815	100%	100%	100%
STM103908	BCE114708	28%	99.6%	99.3%
STM103908	BFU100174	28%	51.3%	97.9%
STM103908	BFU100103	29%	99.6%	99.3%
STM103908	BMA108675	29%	99.6%	99.0%
STM103908	EBC102778	81%	82.2%	94.6%
STM103908	ECO102028	88%	100%	95.5%
STM103908	KPN301730	84%	100%	95.3%
STM103908	PRT101397	53%	100%	100%
STM103908	PAE204868	29%	97.8%	96.0%
STM103908	PPU100478	27%	97.8%	95.5%
STM103908	PSY101023	29%	97.6%	95.7%
STM103908	SPA100063	86%	68.7%	100%
STM103908	STY104171	99%	100%	100%
STM103908	STM103908	100%	100%	100%
STM103908	VCH101366	54%	100%	100%
STM103908	YPS003105	71%	100%	100%
STM103938	ABA104340	34%	47.1%	38.6%
STM103938	BCE100985	29%	51.9%	43.2%
STM103938	BFU111670	34%	47.1%	37.4%
STM103938	BMA108444	33%	51.9%	42.9%
STM103938	EBC101816	63%	99.0%	98.2%
STM103938	ECO102066	80%	100%	64.0%
STM103938	KPN304485	70%	99.0%	98.1%
STM103938	PPU110423	34%	84.6%	83.3%
STM103938	PSY105412	32%	48.1%	51.5%
STM103938	SPA103081	100%	100%	95.4%
STM103938	STY104192	100%	100%	100%
STM103938	STM103938	100%	100%	100%
STM104133	BPT105409	27%	81.1%	76.7%
STM104133	BCE103874	31%	67.7%	49.1%
STM104133	BMA103613	24%	87.6%	98.4%
STM104133	STM104133	100%	100%	100%
STM104223	EFA203072	34%	13.4%	11.1%
STM104223	MLP101303	26%	24.4%	26.9%
STM104223	STM104223	100%	100%	100%
STM104237	STM104237	100%	100%	100%
STM104276	EBC106188	44%	98.6%	84.5%
STM104276	KPN109099	52%	78.6%	75.2%
STM104276	STM104276	100%	100%	100%
STM104686	BCE110467	45%	98.6%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
STM104686	BFU102583	27%	81.8%	78.5%
STM104686	BMA102061	28%	86.5%	72.5%
STM104686	EBC104891	25%	89.2%	89.0%
STM104686	KPN107511	36%	38.5%	58.1%
STM104686	PRT103753	26%	96.6%	98.6%
STM104686	PAE200094	33%	41.9%	43.8%
STM104686	PPU110480	40%	94.6%	80.3%
STM104686	STY104879	100%	100%	100%
STM104686	STM104686	100%	100%	100%
STM104686	YPS004196	35%	94.6%	89.5%

The data in Table IV demonstrates the methods described herein identified genes required for proliferation in several species which share homology.

EXAMPLE 9

Identification of Genes and their Corresponding Operons Affected by Antisense Inhibition

Once the genes involved in *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae* or *Yersinia pestis* proliferation are identified as described above, the operons in which these genes lie may be identified by comparison with known microbial genomes. Since bacterial genes are transcribed in a polycistronic manner, the antisense inhibition of a single gene in an operon might affect the expression of all the other genes on the operon or the genes downstream from the single gene identified. Accordingly, each of the genes contained within an operon may be analyzed for their effect on proliferation.

Operons are predicted by looking for all adjacent genes in a genomic region that lie in the same orientation with no large noncoding gaps in between. First, full-length ORFs complementary to the antisense molecules are identified as described above. Adjacent ORFs are then identified and their relative orientation determined either by directly analyzing the genomic sequences surrounding the ORFs complementary to the antisense clones or by extracting adjacent ORFs from the collection obtained through whole genome ORF analysis described above followed by ORF alignment. Operons predicted in this way may be confirmed by comparison to the arrangement of the homologous nucleic acids in the *Bacillus subtilis* complete genome sequence, as reported by the genome database compiled at Institut Pasteur Subtilist Release R15.1 (June 24, 1999) which can be found at http://bioweb.pasteur.fr/GenoList/SubtiList/. The *Bacillus subtilis* genome is the only fully sequenced and annotated genome from a Gram positive microorganism, and appears to have a high level of similarity to *Staphylococcus aureus* both at the level of conservation of gene sequence and genomic organization including operon structure. Operons for *Salmonella typhimurium* and *Klebsiella pneumoniae* may be identified by comparison with *E. coli, Haemophilus,* or

Pseudomonas sequences. The *Pseudomonas aeruginosa* web site (http://www.pseudomonas.com) can also be used to help predict operon organization in this bacterium.

Extensive DNA sequences of *Salmonella typhimurium* are available through the Salmonella Genome Center (Washington University, St. Louis, MO) the Sanger Centre (United Kingdom) and the PathoSeq database (Incyte). Annotation of some of the DNA sequences in some of the aforementioned databases is lacking, but comparisons may be made to *E. coli* using tools such as BLASTX.

Public or proprietary databases may be used to analyzed *E. faecalis* sequences as well as sequences from the organisms listed above.

The analysis of the operons on which essential genes lie may be conducted for each of the sequences which are listed in Table IA which inhibit proliferation and the ORFs listed in Table IC. Once the full length ORFs and/or the operons containing them have been identified using the methods described above, they can be obtained from a genomic library by performing a PCR amplification using primers at each end of the desired sequence. Those skilled in the art will appreciate that a comparison of the ORFs to homologous sequences in other cells or microorganisms will facilitate confirmation of the start and stop codons at the ends of the ORFs.

In some embodiments, the primers may contain restriction sites which facilitate the insertion of the gene or operon into a desired vector. For example, the gene may be inserted into an expression vector and used to produce the proliferation-required protein as described below. Other methods for obtaining the full length ORFs and/or operons are familiar to those skilled in the art. For exmaple, natural restriction sites may be employed to insert the full length ORFs and/or operons into a desired vector.

EXAMPLE 10

Identification of Individual Genes within an Operon Required for Proliferation

The following example illustrates a method for determining if a targeted gene within an operon is required for cell proliferation by replacing the targeted allele in the chromosome with an in-frame deletion of the coding region of the targeted gene.

Deletion inactivation of a chromosomal copy of a gene in *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi,*

Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae or *Yersinia pestis* can be accomplished by integrative gene replacement. The principles of this method were described in Xia, M., et al. 1999 Plasmid 42:144-149 and Hamilton, C. M., et al 1989. *J. Bacteriol.* **171**: 4617-4622. A similar gene disruption method is available for *Pseudomonas aeruginosa*, except the counter selectable marker is *sacB* (Schweizer, H. P., Klassen, T. and Hoang, T. (1996) Mol. Biol. of *Pseudomonas*. ASM press, 229-237. In this approach, a mutant allele of the targeted gene is constructed by way of an in-frame deletion and introduced into the chromosome using a suicide vector. This results in a tandem duplication comprising a deleted (null) allele and a wild type allele of the target gene. Cells in which the vector sequences have been deleted are isolated using a counter-selection technique. Removal of the vector sequence from the chromosomal insertion results in either restoration of the wild-type target sequence or replacement of the wild type sequence with the deletion (null) allele. *E. faecalis* genes can be disrupted using a suicide vector that contains an internal fragment to a gene of interest. With the appropriate selection this plasmid will homologously recombine into the chromosome (Nallapareddy, S. R., X. Qin, G. M. Weinstock, M. Hook, B. E. Murray. 2000. Infect. Immun. 68:5218-5224.

The resultant population of *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae* or *Yersinia pestis* colonies can then be evaluated to determine whether the target sequence is required for proliferation by PCR amplification of the affected target sequence. If the targeted gene is not required for proliferation, then PCR analysis will show that roughly equal numbers of colonies have retained either the wild-type or the mutant allele. If the targeted gene is required for proliferation, then only wild-type alleles will be recovered in the PCR analysis.

The method of cross-over PCR is used to generate the mutant allele by amplification of nucleotide sequences flanking but not including the coding region of the gene of interest, using specifically designed primers such that overlap between the resulting two PCR amplification

products allows them to hybridize. Further PCR amplification of this hybridization product using primers representing the extreme 5' and 3' ends can produce an amplification product containing an in-frame deletion of the coding region but retaining substantial flanking sequences.

For *Staphylococcus aureus,* this amplification product is subcloned into the suicide vector pSA3182 (Xia, M., et al. 1999 Plasmid 42:144-149, which is host-dependent for autonomous replication. This vector includes a *tetC* tetracycline-resistance marker and the origin of replication of the well-known *Staphylococcus aureus* plasmid pT181 (Mojumdar, M and Kahn, S.A., Characterisation of the Tetracycline Resistance Gene of Plasmid pT181, J. Bacteriol. 170: 5522 (1988). The vector lacks the *repC* gene which is required for autonomous replication of the vector at the pT181 origin. This vector can be propagated in a *Staphylococcus aureus* host strain such as SA3528, which expresses *repC* in trans. Once the amplified truncated target gene sequence is cloned and propagated in the pSA3182 vector, it can then be introduced into a *repC* minus strain such as RN4220 (Kreiswirth, B.N. et al., The Toxic Shock Syndrome Exotoxin Structural Gene is Not Detectably Transmitted by a Prophage, Nature 305:709-712 (1983), by electroporation with selection for tetracycline resistance. In this strain, the vector must integrate by homologous recombination at the targeted gene in the chromosome to impart drug resistance. This results in a inserted truncated copy of the allele, followed by pSA3182 vector sequence, and finally an intact and functional allele of the targeted gene.

Once a tetracycline resistant *Staphylococcus aureus* strain is isolated using the above technique and shown to include truncated and wild-type alleles of the targeted gene as described above, a second plasmid, pSA7592 (Xia, M., et al. 1999 Plasmid 42:144-149, is introduced into the strain by electroporation. This gene includes an erythromycin resistance gene and a *repC* gene that is expressed at high levels. Expression of *repC* in these transformants is toxic due to interference of normal chromosomal replication at the integrated pT181 origin of replication. This selects for strains that have removed the vector sequence by homologous recombination, resulting in either of two outcomes: The selected cells either possess a wild-type allele of the targeted gene or a gene in which the wild-type allele has been replaced by the engineered in-frame deletion of the truncated allele.

PCR amplification can be used to determine the genetic outcome of the above process in the resulting erythromycin resistant, tet sensitive transformant colonies. If the targeted gene is not required for cellular replication, then PCR evidence for both wild-type and mutant alleles will be found among the population of resultant transformants. However, if the targeted gene is required for cellular proliferation, then only the wild-type form of the gene will be evident among the resulting transformants.

Similarly, for *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia*

pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae or *Yersinia pestis* the PCR products containing the mutant allele of the target sequence may be introduced into an appropriate knockout vector and cells in which the wild type target has been disrupted are selected using the appropriate methodology.

The above methods have the advantage that insertion of an in-frame deletion mutation is far less likely to cause downstream polar effects on genes in the same operon as the targeted gene. However, it will be appreciated that other methods for disrupting *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae* or *Yersinia pestis* genes which are familiar to those skilled in the art may also be used.

Each gene in the operon may be disrupted using the methodology above to determine whether it is required for proliferation.

EXAMPLE 11

Expression of the Proteins Encoded by Genes Identified as Required for *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium*

diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Yersinia pestis Proliferation

The following is provided as one exemplary method to express the proliferation-required proteins idenfied as described above. The proliferation-required proteins may be expressed using any of the bacterial, insect, yeast, or mammalian expression systems known in the art. In some embodiments, the proliferation-required proteins encoded by the identified nucleotide sequences described above (including the proteins of SEQ ID NOs.: 42398-78581 encoded by the nucleic acids of SEQ ID NOs.: 6214-42397 are expressed using expression systems designed either for *E. coli* or for *Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae* or *Yersinia pestis*. First, the initiation and termination codons for the gene are identified. If desired, methods for improving translation or expression of the protein are well known in the art. For example, if the nucleic acid encoding the polypeptide to be expressed lacks a methionine codon to serve as the initiation site, a strong Shine-Delgarno sequence, or a stop codon, these nucleotide sequences can be added. Similarly, if the identified nucleic acid lacks a transcription termination signal, this nucleotide sequence can be added to the construct by, for example, splicing out such a sequence from an appropriate donor sequence. In addition, the coding sequence may be operably linked to a strong constitutive promoter or an inducible promoter if desired. The identified nucleic acid or portion thereof encoding the polypeptide to be expressed is obtained by, for example, PCR from the bacterial expression vector or genome using oligonucleotide primers complementary to the identified nucleic acid or portion thereof and containing restriction endonuclease sequences appropriate for inserting the coding sequences into the vector such that the coding sequences can be

expressed from the vector's promoter. Alternatively, other conventional cloning techniques may be used to place the coding sequence under the control of the promoter. In some embodiments, a termination signal may be located downstream of the coding sequence such that transcription of the coding sequence ends at an appropriate position.

Several expression vector systems for protein expression in *E. coli* are well known and available to those knowledgeable in the art. The coding sequence may be inserted into any of these vectors and placed under the control of the promoter. The expression vector may then be transformed into DH5α or some other *E. coli* strain suitable for the over expression of proteins.

Alternatively, an expression vector encoding a protein required for proliferation of *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae* or *Yersinia pestis* may be introduced into *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae* or *Yersinia pestis*. Protocols for introducing nucleic acids into these organisms are well known in the art. For example, the protocols described in J.C.Lee "Electroporation of Staphylococci" from Methods in Molecular Biology vol 47: Electroporation Protocols for Microorganisms Edited by :

J.A. Nickoloff Humana Press Inc., Totowa, NJ. pp209-216, may be used to introduce nucleic acids into *Staphylococcus aureus*. Nucleic acids may also be introduced into *Salmonella typhimurium, Klebsiella pneumoniae, Pseudomonas aeruginosa* or *Enterococcus faecalis* using methods familiar to those skilled in the art. Positive transformants are selected after growing the transformed cells on plates containing an antibiotic to which the vector confers resistance. In one embodiment, *Staphylococcus aureus* is transformed with an expression vector in which the coding sequence is operably linked to the T5 promoter containing a xylose operator such that expression of the encoded protein is inducible with xylose.

In one embodiment, the protein is expressed and maintained in the cytoplasm as the native sequence. In an alternate embodiment, the expressed protein can be modified to include a protein tag that allows for differential cellular targeting, such as to the periplasmic space of Gram negative or Gram positive expression hosts or to the exterior of the cell (i.e., into the culture medium). In some embodiments, the osmotic shock cell lysis method described in Chapter 16 of **Current Protocols in Molecular Biology,** Vol. 2, (Ausubel, et al., Eds.) John Wiley & Sons, Inc. (1997) may be used to liberate the polypeptide from the cell. In still another embodiment, such a protein tag could also facilitate purification of the protein from either fractionated cells or from the culture medium by affinity chromatography. Each of these procedures can be used to express a proliferation-required protein.

Expressed proteins, whether in the culture medium or liberated from the periplasmic space or the cytoplasm, are then purified or enriched from the supernatant using conventional techniques such as ammonium sulfate precipitation, standard chromatography, immunoprecipitation, immunochromatography, size exclusion chromatography, ion exchange chromatography, and HPLC. Alternatively, the polypeptide may be secreted from the host cell in a sufficiently enriched or pure state in the supernatant or growth media of the host cell to permit it to be used for its intended purpose without further enrichment. The purity of the protein product obtained can be assessed using techniques such as SDS PAGE, which is a protein resolving technique well known to those skilled in the art. Coomassie, silver staining or staining with an antibody are typical methods used to visualize the protein of interest.

Antibodies capable of specifically recognizing the protein of interest can be generated using synthetic peptides using methods well known in the art. See, **Antibodies: A Laboratory Manual,** (Harlow and Lane, Eds.) Cold Spring Harbor Laboratory (1988). For example, 15-mer peptides having an amino acid sequence encoded by the appropriate identified gene sequence of interest or portion thereof can be chemically synthesized. The synthetic peptides are injected into mice to generate antibodies to the polypeptide encoded by the identified nucleic acid sequence of interest or portion thereof. Alternatively, samples of the protein expressed from the expression vectors discussed above can be purified and subjected to amino acid sequencing analysis to confirm the identity of the recombinantly expressed protein and subsequently used to raise antibodies. An Example describing in detail the generation of monoclonal and polyclonal antibodies appears in Example 12.

The protein encoded by the identified nucleic acid of interest or portion thereof can be purified using standard immunochromatography techniques. In such procedures, a solution containing the secreted protein, such as the culture medium or a cell extract, is applied to a column having antibodies against the secreted protein attached to the chromatography matrix. The secreted protein is allowed to bind the immunochromatography column. Thereafter, the column is washed to remove non-specifically bound proteins. The specifically-bound secreted protein is then released from the column and recovered using standard techniques. These procedures are well known in the art.

In an alternative protein purification scheme, the identified nucleic acid of interest or portion thereof can be incorporated into expression vectors designed for use in purification schemes employing chimeric polypeptides. In such strategies the coding sequence of the identified nucleic acid of interest or portion thereof is inserted in-frame with the gene encoding the other half of the chimera. The other half of the chimera can be maltose binding protein (MBP) or a nickel binding polypeptide encoding sequence. A chromatography matrix having maltose or nickel attached thereto is then used to purify the chimeric protein. Protease cleavage sites can be engineered between the MBP gene or the nickel binding polypeptide and the identified expected gene of interest, or portion thereof. Thus, the two polypeptides of the chimera can be separated from one another by protease digestion.

One useful expression vector for generating maltose binding protein fusion proteins is pMAL (New England Biolabs), which encodes the *malE* gene. In the pMal protein fusion system, the cloned gene is inserted into a pMal vector downstream from the *malE* gene. This results in the expression of an MBP-fusion protein. The fusion protein is purified by affinity chromatography. These techniques as described are well known to those skilled in the art of molecular biology.

EXAMPLE 12

Production of an Antibody to an isolated *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae* or *Yersinia pestis* Protein

Substantially pure protein or polypeptide (including one of the polypeptides of SEQ ID NOs.: 42398-78581) is isolated from the transformed cells as described in Example 11. The concentration of

protein in the final preparation is adjusted, for example, by concentration on a 10,000 molecular weight cut off AMICON filter device (Millipore, Bedford, MA), to the level of a few micrograms/ml. Monoclonal or polyclonal antibody to the protein can then be prepared as follows:

Monoclonal Antibody Production by Hybridoma Fusion

Monoclonal antibody to epitopes of any of the peptides identified and isolated as described can be prepared from murine hybridomas according to the classical method of Kohler, G. and Milstein, C., **Nature 256**:495 (1975) or any of the well-known derivative methods thereof. Briefly, a mouse is repetitively inoculated with a few micrograms of the selected protein or peptides derived therefrom over a period of a few weeks. The mouse is then sacrificed, and the antibody-producing cells of the spleen isolated. The spleen cells are fused by means of polyethylene glycol with mouse myeloma cells, and the excess unfused cells are destroyed by growth of the system on selective medium comprising aminopterin (HAT medium). The successfully-fused cells are diluted and aliquots of the dilution placed in wells of a microtiter plate where growth of the culture is continued. Antibody-producing clones are identified by detection of antibody in the supernatant fluid of the wells by immunoassay procedures, such as ELISA, as described by Engvall, E., "Enzyme immunoassay ELISA and EMIT," **Meth. Enzymol. 70**:419 (1980), and derivative methods thereof. Selected positive clones can be expanded and their monoclonal antibody product harvested for use. Detailed procedures for monoclonal antibody production are described in Davis, L. et al. **Basic Methods in Molecular Biology** Elsevier, New York. Section 21-2.

Polyclonal Antibody Production by Immunization

Polyclonal antiserum containing antibodies to heterogeneous epitopes of a single protein or a peptide can be prepared by immunizing suitable animals with the expressed protein or peptides derived therefrom described above, which can be unmodified or modified to enhance immunogenicity. Effective polyclonal antibody production is affected by many factors related both to the antigen and the host species. For example, small molecules tend to be less immunogenic than larger molecules and can require the use of carriers and adjuvant. Also, host animals vary in response to site of inoculations and dose, with both inadequate or excessive doses of antigen resulting in low titer antisera. Small doses (ng level) of antigen administered at multiple intradermal sites appears to be most reliable. An effective immunization protocol for rabbits can be found in Vaitukaitis, J. et al. **J. Clin. Endocrinol. Metab. 33**:988-991 (1971).

Booster injections can be given at regular intervals, and antiserum harvested when antibody titer thereof, as determined semi-quantitatively, for example, by double immunodiffusion in agar against known concentrations of the antigen, begins to fall. See, for example, Ouchterlony, O. et al., Chap. 19 in: **Handbook of Experimental Immunology** D. Wier (ed) Blackwell (1973). Plateau concentration of antibody is usually in the range of 0.1 to 0.2 mg/ml of serum (about 12 μM). Affinity of the antisera for the antigen is determined by preparing competitive binding curves, as described, for example, by Fisher, D., Chap. 42 in: **Manual of Clinical Immunology**, 2d Ed. (Rose and Friedman, Eds.) Amer. Soc. For Microbiol., Washington, D.C. (1980).

Antibody preparations prepared according to either protocol are useful in quantitative immunoassays which determine concentrations of antigen-bearing substances in biological samples; they are also used semi-quantitatively or qualitatively to identify the presence of antigen in a biological sample. The antibodies can also be used in therapeutic compositions for killing bacterial cells expressing the protein.

EXAMPLE 13

Construction of Strains Which Overexpress or Underexpress Gene Products Required for Proliferation by Promoter Replacement

Strains which overexpress or underexpress gene products required for proliferation may also be constructed by replacing the promoters which naturally direct transcription of these gene products with promoters which provide the desired level of expression. As described above, such strains are useful in methods for identifying essential genes, in methods for identifying compounds which inhibit cellular proliferation, in methods for identifying the targets of compounds which inhibit proliferation, as well as in methods for identifying genes encoding gene products required for proliferation. Some embodiments of the present invention contemplate the use of a vector that comprises a regulatable fusion promoter selected from a suite of fusion promoters wherein the promoter suite is useful for modulating both the basal and maximal levels of transcription of a nucleic acid over a wide dynamic range thus allowing the desired level of production of a transcript which corresponds to a nucleic acid described herein. Such promoters are described in U.S. Patent Application Serial Number 10/032,393, filed December 21, 2001, the disclosure of which is incorported herein by reference in its entirety.

For example, in some embodiments, the natural promoter may be replaced using techniques which employ homologous recombination to exchange a promoter present on the chromosome of the cell with the desired promoter. In such methodology, a nucleic acid comprising a promoter replacement cassette is introduced into the cell. As illustrated in Figure 1A, the promoter replacement cassette comprises a 5' region homologous to the sequence which is 5' of the natural promoter in the chromosome, the promoter which is to replace the chromosomal promoter and a 3' region which is homologous to sequences 3' of the natural promoter in the chromosome. In some embodiments, the promoter replacement cassette may also include a nucleic acid encoding an identifiable or selectable marker disposed between the 5' region which is homologous to the sequence 5' of the natural promoter and the promoter which is to replace the chromosomal promoter. If desired, the promoter replacement cassette may also contain a transcriptional terminator 3' of the gene encoding an identifiable or selectable marker, as illustrated in Figure 1B. As illustrated in Figure 1A and 1B, homologous recombination is allowed to occur between the chromosomal region containing the natural promoter and the promoter replacement cassette. Cells in which the promoter replacement cassette has integrated into the chromosome are identified or selected. To confirm that homologous recombination has occurred, the chromosomal structure of the cells may be verified by Southern analysis or PCR.

In some embodiments, the promoter replacement cassette may be introduced into the cell as a linear nucleic acid, such a PCR product or a restriction fragment. Alternatively, the promoter replacement may be introduced into the cell on a plasmid. Figures 1A and 1B illustrates the replacement of a chromosomal promoter with a desired promoter through homologous recombination.

In some embodiments, the cell into which the promoter replacement cassette is introduced may carry mutations which enhance its ability to be transformed with linear DNA or which enhance the frequency of homologous recombination. For example, if the cell is an *Escherichia coli* cell it may have a mutation in the gene encoding Exonuclease V of the RecBCD recombination complex. If the cell is an *Escherichia coli* cell it may have a mutation that activates the RecET recombinase of the Rac prophage and/or a mutation that enhances recombination through the RecF pathway. For example, the *Escherichia coli* cells may be RecB or RecC mutants carrying an sbcA or sbcB mutation. Alternatively, the *Escherichia coli* cells may be recD mutants. In other embodiments the *Escherichia coli* cells may express the λ Red recombination genes. For example, *Escherichia coli* cells suitable for use in techniques employing homologous recombination have been described in Datsenko, K.A. and Wanner, B.L., PNAS 97:6640-6645 (2000); Murphy, K.C., J. Bact 180: 2053-2071 (1998); Zhang, Y., et al., Nature Genetics 20: 123-128 (1998); and Muyrers, J.P.P. et al., Genes & Development 14: 1971-1982 (2000). It will be appreciated that cells carrying mutations in similar genes may be constructed in organisms other than *Escherichia coli*.

In some embodiments, the methods described in U.S. Patent Application Serial Number 09/948,993, may be used to place the gene required for proliferation under the control of a regulatable promoter.

If the organism in which promoter replacement is to be performed is diploid, strains in which genes encoding gene products required for proliferation are under the control of a desired promoter may be constructed by inactivating one chromosomal copy of a gene encoding a gene product required for proliferation. For example, the gene may be inactivated by insertion of or replacement by a nucleotide sequence encoding a selectable or detectable gene product, such as a polypeptide which provides resistance to a drug or which allows growth under certain culture conditions. The other chromosomal copy of the gene encoding a gene product required for proliferation is placed under the control of a regulatable promoter, such as the tetracycline regulatable promoter similar to that described in Gari et al., (1997) *Yeast* **13**:837-848 and Nagahashi et al., (1997) *Mol. Gen. Genet.* **255**:372-375, by homologous recombination. The resultant strains may be used to identify genes which encode gene products required for proliferation and in the methods of the present invention.

The method may also be applied to haploid organisms by modifying the single allele of the gene via recombination of the allele with a promoter replacement fragment comprising a nucleotide sequence encoding a heterologous promoter, such that the expression of the gene is conditionally regulated by the heterologous promoter. By repeating this process for a preferred subset of genes in

a haploid pathogenic organism, or its entire genome, a collection or a complete set of conditional mutant strains can be obtained.

It will be appreciated that the means to achieve conditional expression are not restricted to the promoters discussed above and can be performed with other conditional promoters. Such conditional promoter may, for example, be regulated by a repressor which repress transcription from the promoter under particular condition or by a transactivator which increases transcription from the promoter, such as, when in the presence of an inducer.

Although not mandatory, performing the gene disruption first enables heterozygous strains to be constructed and separately collected as a heterozygote strain collection during the process of drug target validation. Heterozygous strains for a given gene express approximately half the normal diploid level of a particular gene product. Consequently, these strains provide constructions having a diminished level of the encoded gene product, and they may be used in the methods described herein. However, it is clear to those skilled in the art that the order of allele modification followed in this embodiment of the invention is not critical, and that it is feasible to perform these steps in a different order such that the conditional-expressing allele is constructed first and the disruption of the remaining wild type gene allele be performed subsequently. However, where the promoter replacement step is carried out first, it is preferable to delete sequences homologous to those employed in the gene disruption step.

Alternatively, conditional expression could be achieved by means other than the reliance of conditional promoters. For example, conditional expression could be achieved by the replacement of the wild type allele in haploid or heterozygous strains with temperature sensitive alleles derived *in vitro,* and their phenotype would then be analyzed at the nonpermissive temperature. In a related approach, in heterozygous strains, insertion of a ubiquitination signal into the remaining wild type allele to destabilize the gene product during activation conditions can be adopted to examine phenotypic effects resulting from gene inactivation.

In another alternative, a constitutive promoter regulated by an excisable transactivator can be used. The promoter is placed upstream to a target gene to repress expression to the basal level characteristic of the promoter. For example, if the strains are fungal organisms, a heterologous promoter containing lexA operator elements may be used in combination with a fusion protein composed of the lexA DNA binding domain and any transcriptional activator domain (*e.g.* GAL4, HAP4, VP16) to provide constitutive expression of a target gene. Counterselection mediated by 5-FOA can be used to select those cells which have excised the gene encoding the fusion protein. This procedure enables an examination of the phenotype associated with repression of the target gene to the basal level of expression provided by the lexA heterologous promoter in the absence of a functional transcription activator. The strains generated by this approach may be used in the present invention.

Alternatively, conditional expression of a target gene can be achieved without the use of a transactivator containing a DNA binding, transcriptional activator domain. A cassette could be

assembled to contain a heterologous constitutive promoter downstream of, for example, the URA3 selectable marker, which is flanked with a direct repeat containing homologous sequences to the 5' portion of the target gene. Additional homologous sequences upstream of the target, when added to this cassette would facilitate homologous recombination and replacement of the native promoter with e above-described heterologous promoter cassette immediately upstream of the start codon of the target gene or open reading frame. Conditional expression is achieved by selecting strains, by using 5-FOA containing media, which have excised the heterologous constitutive promoter and URA3 marker (and consequently lack those regulatory sequences upstream of the target gene required for expression of the gene) and examining the growth of the resulting strain *versus* a wild type strain grown under identical conditions.

EXAMPLE 14

Promoter Replacement to Generate Cells Capable of Overexpressing or Underexpressing a Gene Encoding a Gene Product Required for Proliferation

A target for promoter replacement is selected. A promoter replacement cassette is obtained by inserting a nucleic acid comprising the rrnBT1T2 transcriptional terminator followed by the lac promoter into pACYC184 such that the rrnB terminator and lac promoter are positioned 3' of the CAT gene. The promoter replacement cassette (CAT-rrnBT1T2-plac) is amplified by PCR. The PCR product is used as the template for another round of PCR using primers with 60-80 bp of homology to a target promoter (i.e. a promoter which directs expression of a gene encoding a gene product required for proliferation) and 20 bp of homology to the CAT/rrnBT1T2/plac template as described above. The region of homology is chosen such that upon homologous recombination, the CAT/rrnBT1T2/plac cassette replaces the promoter of the target gene but leaves its Shine-Delgarno motif untouched.

The promoter replacement cassette is transformed into competent JC8679. JC8679 is available from the E. coli genetics stock center. JC8679 allows recombination of short linear DNAs and also contains a lacY mutation which allows titratable regulation of the lac promoter. The transformed cells are plated onto LB/chloramphenicol plates containing various levels of IPTG to assure that the correct level of expression is achieved to allow survival. The correct integration of the promoter replacement cassette is confirmed by colony PCR. If desired, proper regulation of the target gene by the inserted promoter may be confirmed by testing the integrants for growth defects when inducer is absent or present at levels lower than that at which the original colonies were obtained. The inability to grow in the absence of inducer (IPTG) or in the presence of lower levels of the inducer than were used to obtain the clones confirms that the target gene is properly regulated by the inserted promoter. It will be appreciated that although the lac promoter and the strain JC8679 are used as examples, the method may be performed using any suitable regulatable promoter and organism or strain to generate cells which are capable of overexpressing or underexpressing a gene encoding a gene product required for proliferation. Examples of promoters that are useful for the regulating the expression of gene products in Gram-positive organisms over a

wide dynamic range are described in U.S. Patent Application Serial Number 10/032,393, filed December 21, 2001.

The following example describes one method for promoter replacement in a prokaryotic cell. It will be appreciated that promoter replacement can be used in a variety of organisms as previously indicated.

EXAMPLE 15

Operator Insertion to Generate Cells Capable of Overexpressing or Underexpressing a Gene Encoding a Gene Product Required for Proliferation

An oligonucleotide comprising a lac operator flanked on each side by 40 nucleotides homologous to the target promoter is designed. The target promoter is the promoter which drives expression of a gene encoding a gene product required for proliferation, such as the *yabB yabC ftsL ftsI murE* genes in an operon. The sequence of the oligonucleotide (SEQ ID NO. 78582) and locations of the regions homologous to the promoter are illustrated in Figure 6. The sequence of the promoter is also shown with the locations of the -10 and -35 regions indicated (SEQ ID NO. 78583). The single stranded oligonucleotide is transformed into a bacterium expressing the λ Beta and Gam proteins. The cells in the transformation mixture are diluted and plated on medium containing IPTG. Colonies in which the lac operator has integrated into the target promoter are identified by colony PCR. If desired, proper regulation of the target promoter by the inserted operator is confirmed by growing the identified colonies in medium containing or lacking IPTG. The colonies proliferate on medium containing IPTG but fail to grow on medium lacking IPTG, thereby confirming that the target promoter is properly regulated by the inserted operator. It will be appreciated that the preceding method may be performed with any target promoter and any operator to generate cells which overexpress or underexpress a gene encoding a gene product required for proliferation.

EXAMPLE 16

Screening Chemical Libraries

A. Protein-Based Assays

Having isolated and expressed bacterial proteins shown to be required for bacterial proliferation, the present invention further contemplates the use of these expressed target proteins in assays to screen libraries of compounds for potential drug candidates. The generation of chemical libraries is well known in the art. For example, combinatorial chemistry can be used to generate a library of compounds to be screened in the assays described herein. A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building block" reagents. For example, a linear combinatorial chemical library such as a polypeptide library is formed by combining amino acids in every possible combination to yield peptides of a given length. Millions of chemical compounds theoretically can be synthesized through such combinatorial mixings of chemical building blocks. For example, one commentator observed that the systematic, combinatorial mixing of 100 interchangeable

chemical building blocks results in the theoretical synthesis of 100 million tetrameric compounds or 10 billion pentameric compounds. (Gallop et al., "Applications of Combinatorial Technologies to Drug Discovery, Background and Peptide Combinatorial Libraries," *Journal of Medicinal Chemistry,* Vol. **37**, No. 9, 1233-1250 (1994). Other chemical libraries known to those in the art may also be used, including natural product libraries.

Once generated, combinatorial libraries can be screened for compounds that possess desirable biological properties. For example, compounds which may be useful as drugs or to develop drugs would likely have the ability to bind to the target protein identified, expressed and purified as discussed above. Further, if the identified target protein is an enzyme, candidate compounds would likely interfere with the enzymatic properties of the target protein. For example, the enzymatic function of a target protein may be to serve as a protease, nuclease, phosphatase, dehydrogenase, transporter protein, transcriptional enzyme, and any other type of enzyme known or unknown. Thus, the present invention contemplates using the protein products described above to screen combinatorial chemical libraries.

In one example, the target protein is a serine protease and the substrate of the enzyme is known. The present example is directed towards the analysis of libraries of compounds to identify compounds that function as inhibitors of the target enzyme. First, a library of small molecules is generated using methods of combinatorial library formation well known in the art. U.S. Patent Nos. 5,463,564 and 5,574, 656, to Agrafiotis, et al., entitled "System and Method of Automatically Generating Chemical Compounds with Desired Properties," are two such teachings. Then the library compounds are screened to identify those compounds that possess desired structural and functional properties. U.S. Patent No. 5,684,711, also discusses a method for screening libraries.

To illustrate the screening process, the target polypeptide and chemical compounds of the library are combined with one another and permitted to interact with one another. A labeled substrate is added to the incubation. The label on the substrate is such that a detectable signal is emitted from the products of the substrate molecules that result from the activity of the target polypeptide. The emission of this signal permits one to measure the effect of the combinatorial library compounds on the enzymatic activity of target enzymes by comparing it to the signal emitted in the absence of combinatorial library compounds. The characteristics of each library compound are encoded so that compounds demonstrating activity against the enzyme can be analyzed and features common to the various compounds identified can be isolated and combined into future iterations of libraries.

Once a library of compounds is screened, subsequent libraries are generated using those chemical building blocks that possess the features shown in the first round of screen to have activity against the target enzyme. Using this method, subsequent iterations of candidate compounds will possess more and more of those structural and functional features required to inhibit the function of the target enzyme, until a group of enzyme inhibitors with high specificity for the enzyme can be found. These compounds can then be further tested for their safety and efficacy as antibiotics for use in mammals.

It will be readily appreciated that this particular screening methodology is exemplary only. Other methods are well known to those skilled in the art. For example, a wide variety of screening techniques are known for a large number of naturally-occurring targets when the biochemical function of the target protein is known. For example, some techniques involve the generation and use of small peptides to probe and analyze target proteins both biochemically and genetically in order to identify and develop drug leads. Such techniques include the methods described in PCT publications No. WO9935494, WO9819162, WO9954728. Other techniques utilize natural product libraries or libraries of larger molecules such as proteins.

It will be appreciated that the above protein-based assays may be performed with any of the proliferation-required polypeptides from *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae* or *Yersinia pestis* (including the polypeptides of SEQ ID NOs.: 42398-78581) or portions thereof. In addition, the above protein-based assays may be performed with homologous polypeptides or portions thereof.

B. Cell-Based Assays

Current cell-based assays used to identify or to characterize compounds for drug discovery and development frequently depend on detecting the ability of a test compound to modulate the activity of a target molecule located within a cell or located on the surface of a cell. An advantage of cell-based assays is that they allow the effect of a compound on a target molecule's activity to be detected within the physiologically relevant environment of the cell as opposed to an *in vitro* environment. Most often such target molecules are proteins such as enzymes, receptors and the like. However, target molecules may also include other molecules such as DNAs, lipids, carbohydrates and RNAs including messenger RNAs, ribosomal RNAs, tRNAs, regulatory RNAs and the like. A number of highly sensitive cell-based assay methods are available to those of skill in the art to detect binding and interaction of test compounds with specific target molecules. However, these methods are generally not highly effective when the test compound binds to or otherwise interacts with its target molecule with moderate or low affinity. In addition, the target molecule may not be

readily accessible to a test compound in solution, such as when the target molecule is located inside the cell or within a cellular compartment. Thus, current cell-based assay methods are limited in that they are not effective in identifying or characterizing compounds that interact with their targets with moderate to low affinity or compounds that interact with targets that are not readily accessible.

The cell-based assay methods of the present invention have substantial advantages over current cell-based assays. These advantages derive from the use of sensitized cells in which the level or activity of at least one proliferation-required gene product (the target molecule) has been specifically reduced to the point where the presence or absence of its function becomes a rate-determining step for cellular proliferation. Bacterial, fungal, plant, or animal cells can all be used with the present method. Such sensitized cells become much more sensitive to compounds that are active against the affected target molecule. Thus, cell-based assays of the present invention are capable of detecting compounds exhibiting low or moderate potency against the target molecule of interest because such compounds are substantially more potent on sensitized cells than on non-sensitized cells. The effect may be such that a test compound may be two to several times more potent, at least 10 times more potent, at least 20 times more potent, at least 50 times more potent, at least 100 times more potent, at least 1000 times more potent, or even more than 1000 times more potent when tested on the sensitized cells as compared to the non-sensitized cells. The proliferation-required nucleic acids or polypeptides from *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae* or *Yersinia pestis,* or portions thereof, may be employed in any of the cell-based assays described herein. Similarly, homologous coding nucleic acids, homologous antisense nucleic acids, or homologous polypeptides or portions of the homologous nucleic acids or homologous polypeptides, may be employed in any of the cell-based assays described herein.

Due in part to the increased appearance of antibiotic resistance in pathogenic microorganisms and to the significant side-effects associated with some currently used antibiotics, novel antibiotics acting at new targets are highly sought after in the art. Yet, another limitation in the current art related to cell-based assays is the problem of repeatedly identifying hits against the

same kinds of target molecules in the same limited set of biological pathways. This may occur when compounds acting at such new targets are discarded, ignored or fail to be detected because compounds acting at the "old" targets are encountered more frequently and are more potent than compounds acting at the new targets. As a result, the majority of antibiotics in use currently interact with a relatively small number of target molecules within an even more limited set of biological pathways.

The use of sensitized cells of the current invention provides a solution to the above problem in two ways. First, desired compounds acting at a target of interest, whether a new target or a previously known but poorly exploited target, can now be detected above the "noise" of compounds acting at the "old" targets due to the specific and substantial increase in potency of such desired compounds when tested on the sensitized cells of the current invention. Second, the methods used to sensitize cells to compounds acting at a target of interest may also sensitize these cells to compounds acting at other target molecules within the same biological pathway. For example, expression of an antisense molecule to a gene encoding a ribosomal protein is expected to sensitize the cell to compounds acting at that ribosomal protein and may also sensitize the cells to compounds acting at any of the ribosomal components (proteins or rRNA) or even to compounds acting at any target which is part of the protein synthesis pathway. Thus an important advantage of the present invention is the ability to reveal new targets and pathways that were previously not readily accessible to drug discovery methods.

Sensitized cells of the present invention are prepared by reducing the activity or level of a target molecule. The target molecule may be a gene product, such as an RNA or polypeptide produced from the proliferation-required nucleic acids from *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae* or *Yersinia pestis* (including a gene product produced from the nucleic acids of SEQ ID NOs.: 6214-42397, such as the polypeptides of SEQ ID NOs.: 42398-78581) or from homologous nucleic acids. For example, the target molecule may be one of the polypeptides of SEQ ID NOs. 42398-78581 or a homologous polypeptide. Alternatively, the target

may be a gene product such as an RNA or polypeptide which is produced from a sequence within the same operon as the proliferation-required nucleic acids *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae* or *Yersinia pestis* or from homologous nucleic acids. In addition, the target may be an RNA or polypeptide in the same biological pathway as the proliferation-required nucleic acids from *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae* or *Yersinia pestis* or from homologous nucleic acids. Such biological pathways include, but are not limited to, enzymatic, biochemical and metabolic pathways as well as pathways involved in the production of cellular structures such as the cell wall.

Current methods employed in the arts of medicinal and combinatorial chemistries are able to make use of structure-activity relationship information derived from testing compounds in various biological assays including direct binding assays and cell-based assays. Occasionally compounds are directly identified in such assays that are sufficiently potent to be developed as drugs. More often, initial hit compounds exhibit moderate or low potency. Once a hit compound is identified with low or moderate potency, directed libraries of compounds are synthesized and tested

in order to identify more potent leads. Generally these directed libraries are combinatorial chemical libraries consisting of compounds with structures related to the hit compound but containing systematic variations including additions, subtractions and substitutions of various structural features. When tested for activity against the target molecule, structural features are identified that either alone or in combination with other features enhance or reduce activity. This information is used to design subsequent directed libraries containing compounds with enhanced activity against the target molecule. After one or several iterations of this process, compounds with substantially increased activity against the target molecule are identified and may be further developed as drugs. This process is facilitated by use of the sensitized cells of the present invention since compounds acting at the selected targets exhibit increased potency in such cell-based assays, thus; more compounds can now be characterized providing more useful information than would be obtained otherwise.

Thus, it is now possible using cell-based assays of the present invention to identify or characterize compounds that previously would not have been readily identified or characterized including compounds that act at targets that previously were not readily exploited using cell-based assays. The process of evolving potent drug leads from initial hit compounds is also substantially improved by the cell-based assays of the present invention because, for the same number of test compounds, more structure-function relationship information is likely to be revealed.

The method of sensitizing a cell entails selecting a suitable gene or operon. A suitable gene or operon is one whose transcription and/or expression is required for the proliferation of the cell to be sensitized. The next step is to introduce into the cells to be sensitized, an antisense RNA capable of hybridizing to the suitable gene or operon or to the RNA encoded by the suitable gene or operon. Introduction of the antisense RNA can be in the form of a vector in which antisense RNA is produced under the control of an inducible promoter. The amount of antisense RNA produced is modulated by varying an inducer concentration to which the cell is exposed and thereby varying the activity of the promoter driving transcription of the antisense RNA. Thus, cells are sensitized by exposing them to an inducer concentration that results in a sub-lethal level of antisense RNA expression. The requisite amount of inducer may be derived empiracally by one of skill in the art.

In one embodiment of the cell-based assays, antisense nucleic acids complementary to the identified *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria*

meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae or *Yersinia pestis* nucleotide sequences or portions thereof (including antisense nucleic acids comprising a nucleotide sequence complementary to one of SEQ ID NOs.: 6214-42397, and the antisense nucleic acids of SEQ ID NOs.: 1-6213 or antisense nucleic acids comprising a nucleotide sequence complementary to portions of the foregoing nucleic acids thereof), antisense nucleic complementary to homologous coding nucleic acids or portions thereof or homologous antisense nucleic acids are used to inhibit the production of a proliferation-required protein. Vectors producing antisense RNA complementary to identified genes required for proliferation, or portions thereof, are used to limit the concentration of a proliferation-required protein without severely inhibiting growth. The proliferation-required protein may be one of the proteins of SEQ ID NOs.: 42398-78581 or a homologous polypeptide. To achieve that goal, a growth inhibition dose curve of inducer is calculated by plotting various doses of inducer against the corresponding growth inhibition caused by the antisense expression. From this curve, the concentration of inducer needed to achieve various percentages of antisense induced growth inhibition, from 1 to 100% can be determined.

In some embodiments of the present invention, promoter replacement methods, such as those describe above and in U.S. Patent Application Serial Number 09/948,993, are used to express the proliferation-inhibiting nucleic acid. In other embodiments, the methods for the production of stabilized RNA in Gram-negative organisms, as described in U.S. Provisional Patent Application Serial Number 60/343,512, are used for the production of proliferation-inhibiting transcripts corresponding to the nucleic acid sequences described herein. Briefly, the stabilized antisense RNA may comprise an antisense RNA which was identified as inhibiting proliferation as described above which has been engineered to contain at least one stem loop flanking each end of the antisense nucleic acid. In some embodiments, the at least one stem-loop structure formed at the 5' end of the stabilized antisense nucleic acid comprises a flush, double stranded 5' end. In some embodiments, one or more of the stem loops comprises a rho independent terminator. In additional embodiments, the stabilized antisense RNA lacks a ribosome binding site. In further embodiments, the stabilized RNA lacks sites which are cleaved by one or more RNAses, such as RNAse E or RNAse III. In some embodiments, the stabilized antisense RNA may be transcribed in a cell which the activity of at least one enzyme involved in RNA degradation has been reduced. For example, the activity of an enzyme such as RNase E, RNase II, RNase III, polynucleotide phosphorylase, and poly(A) polymerase, RNA helicase, enolase or an enzyme having similar functions may be reduced in the cell.

A variety of different regulatable promoters may be used to produce the antisense nucleic acid. Transcription from the regulatable promoters may be modulated by controlling the activity of a transcription factor repressor which acts at the regulatable promoter. For example, if transcription

is modulated by affecting the activity of a repressor, the choice of inducer to be used depends on the repressor/operator responsible for regulating transcription of the antisense nucleic acid. If the regulatable promoter comprises a T5 promoter fused to a *xylO* (xylose operator; e.g. derived from *Staphylococcus xylosis* (Schnappinger, D. et al., FEMS Microbiol. Let. 129: 126214-423978 (1995), then transcription of the antisense nucleic acid may be regulated by a xylose repressor. The xylose repressor may be provided by ectoptic expression within an *S. aureus* cell of an exogenous xylose repressor gene, e.g. derived from *S. xylosis* DNA. In such cases transcription of antisense RNA from the promoter is inducible by adding xylose to the medium and the promoter is thus "xylose inducible." Similarly, IPTG inducible promoters may be used. For example, the highest concentration of the inducer that does not reduce the growth rate significantly can be estimated from the curve. Cellular proliferation can be monitored by growth medium turbidity via OD measurements. In another example, the concentration of inducer that reduces growth by 25% can be predicted from the curve. In still another example, a concentration of inducer that reduces growth by 50% can be calculated. Additional parameters such as colony forming units (cfu) can be used to measure cellular viability. Some embodiments of the present invention contemplate the use of a vector that comprises a regulatable fusion promoter selected from a suite of fusion promoters wherein the promoter suite is useful for modulating both the basal and maximal levels of transcription of a nucleic acid over a wide dynamic range thus allowing the desired level of production of a transcript which corresponds to a nucleic acid described herein. Such promoters are described in U.S. Patent Application Serial Number 10/032,393, filed December 21, 2001, the disclosure of which is incorported herein by reference in its entirety.

Cells to be assayed are exposed to the above-determined concentrations of inducer. The presence of the inducer at this sub-lethal concentration reduces the amount of the proliferation required gene product to a sub-optimal amount in the cell that will still support growth. Cells grown in the presence of this concentration of inducer are therefore specifically more sensitive to inhibitors of the proliferation-required protein or RNA of interest or to inhibitors of proteins or RNAs in the same biological pathway as the proliferation-required protein or RNA of interest but not to inhibitors of unrelated proteins or RNAs.

Cells pretreated with sub-inhibitory concentrations of inducer and thus containing a reduced amount of proliferation-required target gene product are then used to screen for compounds that reduce cell growth. The sub-lethal concentration of inducer may be any concentration consistent with the intended use of the assay to identify candidate compounds to which the cells are more sensitive. For example, the sub-lethal concentration of the inducer may be such that growth inhibition is at least about 5%, at least about 8%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60% at least about 75%, or more. Cells which are pre-sensitized using the preceding method are more sensitive to inhibitors of the target protein because these cells contain less target protein to inhibit than do wild-type cells.

It will be appreciated that the above cell-based assays may be performed using antisense nucleic acids comprising a nucleotide sequence complementary to any of the proliferation-required nucleic acids from *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae* or *Yersinia pestis* or portions thereof, antisense nucleic acids complementary to homologous coding nucleic acids or portions thereof or homologous antisense nucleic acids. In this way, the level or activity of a target, such as any of the proliferation-required polypeptides from *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae* or *Yersinia pestis* or homologous polypeptides.

In another embodiment of the cell-based assays of the present invention, the level or activity of a proliferation required gene product is reduced using a mutation, such as a temperature sensitive mutation, in the gene encoding a gene product required for proliferation and an antisense nucleic acid comprising a nucleotide sequence complementary to the gene encoding the gene product required for proliferation or a portion thereof. Growing the cells at an intermediate temperature between the permissive and restrictive temperatures of the temperature sensitive mutant where the mutation is in a proliferation-required gene produces cells with reduced activity

of the proliferation-required gene product. The antisense RNA complementary to the proliferation-required sequence further reduces the activity of the proliferation required gene product. Drugs that may not have been found using either the temperature sensitive mutation or the antisense nucleic acid alone may be identified by determining whether cells in which transcription of the antisense nucleic acid has been induced and which are grown at a temperature between the permissive temperature and the restrictive temperature are substantially more sensitive to a test compound than cells in which expression of the antisense nucleic acid has not been induced and which are grown at a permissive temperature. Also drugs found previously from either the antisense nucleic acid alone or the temperature sensitive mutation alone may have a different sensitivity profile when used in cells combining the two approaches, and that sensitivity profile may indicate a more specific action of the drug in inhibiting one or more activities of the gene product.

Temperature sensitive mutations may be located at different sites within the gene and correspond to different domains of the protein. For example, the *dnaB* gene of *Escherichia coli* encodes the replication fork DNA helicase. DnaB has several domains, including domains for oligomerization, ATP hydrolysis, DNA binding, interaction with primase, interaction with DnaC, and interaction with DnaA [(Biswas, E.E. and Biswas, S.B. 1999. Mechanism and DnaB helicase of *Escherichia coli*: structural domains involved in ATP hydrolysis, DNA binding, and oligomerization. Biochem. **38**:10919-10928; Hiasa, H. and Marians, K.J. 1999. Initiation of bidirectional replication at the chromosomal origin is directed by the interaction between helicase and primase. J. Biol. Chem. **274**:27244-27248; San Martin, C., Radermacher, M., Wolpensinger, B., Engel, A., Miles, C.S., Dixon, N.E., and Carazo, J.M. 1998. Three-dimensional reconstructions from cryoelectron microscopy images reveal an intimate complex between helicase DnaB and its loading partner DnaC. Structure **6**:501-9; Sutton, M.D., Carr, K.M., Vicente, M., and Kaguni, J.M. 1998. *Escherichia coli* DnaA protein. The N-terminal domain and loading of DnaB helicase at the *E. coli* chromosomal origin. J. Biol. Chem. **273**:34255-62.). Temperature sensitive mutations in different domains of DnaB confer different phenotypes at the restrictive temperature, which include either an abrupt stop or slow stop in DNA replication with or without DNA breakdown (Wechsler, J.A. and Gross, J.D. 1971. *Escherichia coli* mutants temperature-sensitive for DNA synthesis. Mol. Gen. Genetics **113**:273-284, and termination of growth or cell death. Combining the use of temperature sensitive mutations in the *dnaB* gene that cause cell death at the restrictive temperature with an antisense to the *dnaB* gene could lead to the discovery of very specific and effective inhibitors of one or a subset of activities exhibited by DnaB.

It will be appreciated that the above method may be performed with any mutation which reduces but does not eliminate the activity or level of the gene product which is required for proliferation.

It will be appreciated that the above cell-based assays may be performed using mutations in, such as temperature sensitive mutations, and antisense nucleic acids comprising a nucleotide sequence complementary to any of the genes encoding proliferation-required gene products from

from *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae* or *Yersinia pestis* or portions thereof (including the nucleic acids of SEQ ID NOs.: 6214-42397), mutations in and antisense nucleic acids complementary to homologous coding nucleic acids or portions thereof or homologous antisense nucleic acids. In this way, the level or activity of a target, such as any of the proliferation-required polypeptides from *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae* or *Yersinia pestis* (including the polypeptides of SEQ ID NOs.: 42398-78581), or homologous polypeptides may be reduced.

When screening for antimicrobial agents against a gene product required for proliferation, growth inhibition of cells containing a limiting amount of that proliferation-required gene product can be assayed. Growth inhibition can be measured by directly comparing the amount of growth, measured by the optical density of the growth medium, between an experimental sample and a control sample. Alternative methods for assaying cell proliferation include measuring the signal from a reporter construct, various enzymatic activity assays, and other methods well known in the art.

It will be appreciated that the above method may be performed in solid phase, liquid phase or a combination of the two. For example, cells grown on nutrient agar containing the inducer of the antisense construct may be exposed to compounds spotted onto the agar surface. If desired, the cells may be grown on agar containing varying concentrations of the inducer. A compound's effect may be judged from the diameter of the resulting killing zone, the area around the compound application point in which cells do not grow. Multiple compounds may be transferred to agar plates and simultaneously tested using automated and semi-automated equipment including but not restricted to multi-channel pipettes (for example the Beckman Multimek) and multi-channel spotters (for example the Genomic Solutions Flexys). In this way multiple plates and thousands to millions of compounds may be tested per day.

The compounds may also be tested entirely in liquid phase using microtiter plates as described below. Liquid phase screening may be performed in microtiter plates containing 96, 384, 1536 or more wells per microtiter plate to screen multiple plates and thousands to millions of compounds per day. Automated and semi-automated equipment may be used for addition of reagents (for example cells and compounds) and determination of cell density.

EXAMPLE 17

Cell-Based Assay Using Antisense Complementary to Genes Encoding Ribosomal Proteins

The effectiveness of the above cell-based assay was validated using constructs transribing antisense RNA to the proliferation required *E. coli* genes *rplL*, *rplJ*, and *rplW* encoding ribosomal proteins L7/L12, L10 and L23 respectively. These proteins are essential components of the protein synthesis apparatus of the cell and as such are required for proliferation. These constructs were used to test the effect of antisense transcription on cell sensitivity to antibiotics known to bind to the ribosome and thereby inhibit protein synthesis. Constructs transcribing antisense RNA to several other genes (*elaD*, *visC*, *yohH*, and *atpE/B*), the products of which are not involved in protein synthesis were used for comparison.

First, pLex5BA (Krause et al., J. Mol. Biol. 274: 365 (1997), vectors containing antisense constructs to either *rplW* or to *elaD* were introduced into separate *E. coli* cell populations. Vector introduction is a technique well known to those of ordinary skill in the art. The vectors of this example contain IPTG inducible promoters that drive the transcription of the antisense RNA in the presence of the inducer. However, those skilled in the art will appreciate that other inducible promoters may also be used. Suitable vectors are also well known in the art. For example, a number of promoters useful for nucleic acid transcription (including the nucleic acids described herein) in *Enterococcus faecalis, Staphylococcus areus* as well as other Gram positive organisms are described in U.S. Patent Application Serial Number 10/032,393, filed December 21, 2001. Antisense clones to genes encoding different ribosomal proteins or to genes encoding proteins that are not involved in protein synthesis were utilized to test the effect of antisense transcription on cell sensitivity to the antibiotics known to bind to ribosomal proteins and inhibit protein synthesis. Antisense nucleic acids comprising a nucleotide sequence complementarty to the *elaD*, *atpB&atpE*,

visC and *yohH* genes are referred to as AS-*elaD*, AS-*atpB/E*, AS-*visC*, AS-*yohH* respectively. These genes are not known to be involved in protein synthesis. Antisense nucleic acids to the *rplL*, *rplL&rplJ* and *rplW* genes are referred to as AS-*rplL*, AS-*rplL/J*, and AS-*rplW* respectively. These genes encode ribosomal proteins L7/L12 (*rplL*) L10 (*rplJ*) and L23 (*rplW*). Vectors containing these antisense nucleic acids were introduced into separate *E. coli* cell populations.

The cell populations containing vectors producing AS-*elaD* or AS-*rplW* were exposed to a range of IPTG concentrations in liquid medium to obtain the growth inhibitory dose curve for each clone (Figure 7). First, seed cultures were grown to a particular turbidity measured by the optical density (OD) of the growth solution. The OD of the solution is directly related to the number of bacterial cells contained therein. Subsequently, sixteen 200 µl liquid medium cultures were grown in a 96 well microtiter plate at 37° C with a range of IPTG concentrations in duplicate two-fold serial dilutions from 1600 uM to 12.5 µM (final concentration). Additionally, control cells were grown in duplicate without IPTG. These cultures were started from an inoculum of equal amounts of cells derived from the same initial seed culture of a clone of interest. The cells were grown for up to 15 hours and the extent of growth was determined by measuring the optical density of the cultures at 600 nm. When the control culture reached mid-log phase the percent growth (relative to the control culture) for each of the IPTG containing cultures was plotted against the log concentrations of IPTG to produce a growth inhibitory dose response curve for the IPTG. The concentration of IPTG that inhibits cell growth to 50% (IC_{50}) as compared to the 0 mM IPTG control (0% growth inhibition) was then calculated from the curve. Under these conditions, an amount of antisense RNA was produced that reduced the expression levels of *rplW* or *elaD* to a degree such that growth of cells containing their respective antisense vectors was inhibited by 50%.

Alternative methods of measuring growth are also contemplated. Examples of these methods include measurements of proteins, the expression of which is engineered into the cells being tested and can readily be measured. Examples of such proteins include luciferase and various enzymes.

Cells were pretreated with the selected concentration of IPTG and then used to test the sensitivity of cell populations to tetracycline, erythromycin and other known protein synthesis inhibitors. Figure 7 is an IPTG dose response curve in *E. coli* transformed with an IPTG-inducible plasmid containing either an antisense clone to the *E. coli rplW* gene (AS-*rplW*) which encodes ribosomal protein L23 which is required for protein synthesis and essential for cell proliferation, or an antisense clone to the *elaD* (AS-*elaD*) gene which is not known to be involved in protein synthesis.

An example of a tetracycline dose response curve is shown in Figures 8A and 13B for the *rplW* and *elaD* genes, respectively. Cells were grown to log phase and then diluted into medium alone or medium containing IPTG at concentrations which give 20% and 50% growth inhibition as determined by IPTG dose response curves. After 2.5 hours, the cells were diluted to a final OD_{600} of 0.002 into 96 well plates containing (1) +/- IPTG at the same concentrations used for the 2.5 hour

pre-incubation; and (2) serial two-fold dilutions of tetracycline such that the final concentrations of tetracycline range from 1 μg/ml to 15.6 ng/ml and 0 μg/ml. The 96 well plates were incubated at 37°C and the OD_{600} was read by a plate reader every 5 minutes for up to 15 hours. For each IPTG concentration and the no IPTG control, tetracycline dose response curves were determined when the control (absence of tetracycline) reached 0.1 OD_{600}.

To compare tetracycline sensitivity with and without IPTG, tetracycline IC_{50s} were determined from the dose response curves (Figures 8A-B). Cells transcribing antisense nucleic acids AS-*rplL* or AS-*rplW* to genes encoding ribosomal proteins L7/L12 and L23 respectively showed increased sensitivity to tetracycline (Figure 8A) as compared to cells with reduced levels of the *elaD* gene product (AS-*elaD)* (Figure 8B). Figure 9 shows a summary bar chart in which the ratios of tetracycline IC_{50s} determined in the presence of IPTG which gives 50% growth inhibition versus tetracycline IC_{50s} determined without IPTG (fold increase in tetracycline sensitivity) were plotted. Cells with reduced levels of either L7/L12 (encoded by genes *rplL, rplJ*) or L23 (encoded by the *rplW* gene) showed increased sensitivity to tetracycline (Figure 9). Cells expressing antisense to genes not known to be involved in protein synthesis (AS-*atpB/E*, AS-*visC*, AS-*elaD*, AS-*yohH*) did not show the same increased sensitivity to tetracycline, validating the specificity of this assay (Figure 9).

In addition to the above, it has been observed in initial experiments that clones transcribing antisense RNA to genes involved in protein synthesis (including genes encoding ribosomal proteins L7/L12 & L10, L7/L12 alone, L22, and L18, as well as genes encoding rRNA and Elongation Factor G) have increased sensitivity to the macrolide, erythromycin, whereas clones transcribing antisense to the non-protein synthesis genes *elaD, atpB/E* and *visC* do not. Furthermore, the clone transcribing antisense to *rplL* and *rplJ* (AS-*rplL/J)* does not show increased sensitivity to nalidixic acid and ofloxacin, antibiotics which do not inhibit protein synthesis.

The results with the ribosomal protein genes *rplL, rplJ*, and *rplW* as well as the initial results using various other antisense clones and antibiotics show that limiting the concentration of an antibiotic target makes cells more sensitive to the antimicrobial agents that specifically interact with that protein. The results also show that these cells are sensitized to antimicrobial agents that inhibit the overall function in which the protein target is involved but are not sensitized to antimicrobial agents that inhibit other functions. It will be appreciated that the cell-based assays described above may be implemented using the *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis,*

Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae or *Yersinia pestis* antisense nucleotide sequences which inhibit the activity of genes required for proliferation described herein (including the antisense nucleic acids of SEQ ID NOs.: 1-6213) or antisense nucleic acids comprising nucleotide sequences which are complementary to the sequences of SEQ ID NOs.: 6214-42397 or portions thereof.

It will be appreciated that the above cell-based assays may be performed using antisense nucleic acids complementary to any of the proliferation-required nucleic acids from *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae* or *Yersinia pestis* or portions thereof, antisense nucleic acids complementary to homologous coding nucleic acids or portions thereof, or homologous antisense nucleic acids. In this way, the level or activity of a target, such as any of the proliferation-required polypeptides from *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae,*

Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae or *Yersinia pestis* or homologous polypeptides may be reduced.

In some embodiments of the present invention, the methods for the production of stabilized RNA, as described in U.S. Provisional Patent Application Serial Number 60/343,512, can be used in the above cell-based assays in Gram-negative organisms to extend the lifetime of transcripts corresponding to the nucleic acids described herein.

The cell-based assay described above may also be used to identify the biological pathway in which a proliferation-required nucleic acid or its gene product lies. In such methods, cells transcribing a sub-lethal level of antisense to a target proliferation-required nucleic acid and control cells in which transcription of the antisense has not been induced are contacted with a panel of antibiotics known to act in various pathways. If the antibiotic acts in the pathway in which the target proliferation-required nucleic acid or its gene product lies, cells in which transcription of the antisense has been induced will be more sensitive to the antibiotic than cells in which expression of the antisense has not been induced.

As a control, the results of the assay may be confirmed by contacting a panel of cells transcribing antisense nucleic acids to many different proliferation-required genes including the target proliferation-required gene. If the antibiotic is acting specifically, heightened sensitivity to the antibiotic will be observed only in the cells transcribing antisense to a target proliferation-required gene (or cells expressing antisense to other proliferation-required genes in the same pathway as the target proliferation-required gene) but will not be observed generally in all cells expressing antisense to proliferation-required genes.

It will be appreciated that the above cell-based assays may be performed using antisense nucleic acids complementary to any of the proliferation-required nucleic acids from *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae* or *Yersinia pestis* (including antisense nucleic acids complementary to SEQ ID NOs: 6214-42397, or the antisense nucleic acids of SEQ ID NOs.: 1-6213) or portions thereof, antisense nucleic acids comprising nucleotide sequences complementary to homologous

coding nucleic acids or portions thereof, or homologous antisense nucleic acids In this way, the level or activity of a target, such as any of the proliferation-required polypeptides from *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae* or *Yersinia pestis* (including the polypeptides of SEQ ID NOs.: 42398-78581), or homologous polypeptides may be reduced.

In some embodiments of the present invention, the methods for the production of stabilized RNA, as described in U.S. Provisional Patent Application Serial Number 60/343,512, can be used in the above cell-based assays in Gram-negative organisms to extend the lifetime of transcripts corresponding to the nucleic acids described herein.

Similarly, the above method may be used to determine the pathway on which a test compound, such as a test antibiotic acts. A panel of cells, each of which transcribes an antisense to a proliferation-required nucleic acid in a known pathway, is contacted with a compound for which it is desired to determine the pathway on which it acts. The sensitivity of the panel of cells to the test compound is determined in cells in which transcription of the antisense has been induced and in control cells in which expression of the antisense has not been induced. If the test compound acts on the pathway on which an antisense nucleic acid acts, cells in which expression of the antisense has been induced will be more sensitive to the compound than cells in which expression of the antisense has not been induced. In addition, control cells in which expression of antisense to proliferation-required genes in other pathways has been induced will not exhibit heightened sensitivity to the compound. In this way, the pathway on which the test compound acts may be determined.

It will be appreciated that the above cell-based assays may be performed using antisense nucleic acids comprising nucleotide sequences complementary to any of the proliferation-required nucleic acids from *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia*

pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae or *Yersinia pestis* (including antisense nucleic acids complementary to SEQ ID NOs: 6214-42397, such as the antisense nucleic acids of SEQ ID NOs.: 1-6213) or portions thereof, antisense nucleic acids complementary to homologous coding nucleic acids or portions thereof, or homologous antisense nucleic acids In this way, the level or activity of a target, such as any of the proliferation-required polypeptides from *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae* or *Yersinia pestis* (including the polypeptides of SEQ ID NOs.: 42398-78581) or homologous polypeptides may be reduced.

In some embodiments of the present invention, the methods for the production of stabilized RNA, as described in U.S. Provisional Patent Application Serial Number 60/343,512, can be used in the above cell-based assays in Gram-negative organisms to extend the lifetime of transcripts corresponding to the nucleic acids described herein.

The Example below provides one method for performing such assays.

EXAMPLE 18

Identification of the Pathway in which a Proliferation-Required Gene Lies or the Pathway on which an Antibiotic Acts

A. Preparation of Bacterial Stocks for Assay

To provide a consistent source of cells to screen, frozen stocks of host bacteria containing the desired antisense construct are prepared using standard microbiological techniques. For example, a single clone of the microorganism can be isolated by streaking out a sample of the original stock onto an agar plate containing nutrients for cell growth and an antibiotic for which the antisense construct contains a selectable marker which confers resistance. After overnight growth an isolated colony is picked from the plate with a sterile needle and transferred to an appropriate liquid growth medium containing the antibiotic required for maintenance of the plasmid. The cells are incubated at 30°C to 37°C with vigorous shaking for 4 to 6 hours to yield a culture in exponential growth. Sterile glycerol is added to 15% (volume to volume) and 100μL to 500 μL aliquots are distributed into sterile cryotubes, snap frozen in liquid nitrogen, and stored at -80°C for future assays.

B. Growth of Bacteria for Use in the Assay

A day prior to an assay, a stock vial is removed from the freezer, rapidly thawed (37°C water bath) and a loop of culture is streaked out on an agar plate containing nutrients for cell growth and an antibiotic to which the selectable marker of the antisense construct confers resistance. After overnight growth at 37°C, ten randomly chosen, isolated colonies are transferred from the plate (sterile inoculum loop) to a sterile tube containing 5 mL of LB medium containing the antibiotic to which the antisense vector confers resistance. After vigorous mixing to form a homogeneous cell suspension, the optical density of the suspension is measured at 600 nm (OD_{600}) and if necessary an aliquot of the suspension is diluted into a second tube of 5 mL, sterile, LB medium plus antibiotic to achieve an $OD_{600} \leq 0.02$ absorbance units. The culture is then incubated at 37° C for 1-2 hrs with shaking until the OD_{600} reaches OD 0.2 – 0.3. At this point the cells are ready to be used in the assay.

C. Selection of Media to be Used in Assay

Two-fold dilution series of the inducer are generated in culture media containing the appropriate antibiotic for maintenance of the antisense construct. Several media are tested side by side and three to four wells are used to evaluate the effects of the inducer at each concentration in each media. For example, LB broth, TBD broth and Muller-Hinton media may be tested with the inducer xylose at the following concentrations, 5 mM, 10 mM, 20 mM, 40 mM, 80 mM, 120 mM and 160 mM. Equal volumes of test media-inducer and cells are added to the wells of a 384 well microtiter plate and mixed. The cells are prepared as described above and diluted 1:100 in the appropriate media containing the test antibiotic immediately prior to addition to the microtiter plate wells. For a control, cells are also added to several wells of each media that do not contain inducer, for example 0 mM xylose. Cell growth is monitored continuously by incubation at 37°C in a microtiter plate reader monitoring the OD_{600} of the wells over an 18-hour period. The percent inhibition of growth produced by each concentration of inducer is calculated by comparing the rates of logarithmic growth against that exhibited by cells growing in medium without inducer. The medium yielding greatest sensitivity to inducer is selected for use in the assays described below.

D. Measurement of Test Antibiotic Sensitivity in the Absence of Antisense Construct Induction

Two-fold dilution series of antibiotics of known mechanism of action are generated in the culture medium selected for further assay development that has been supplemented with the antibiotic used to maintain the construct. A panel of test antibiotics known to act on different pathways is tested side by side with three to four wells being used to evaluate the effect of a test antibiotic on cell growth at each concentration. Equal volumes of test antibiotic and cells are added to the wells of a 384 well microtiter plate and mixed. Cells are prepared as described above using the medium selected for assay development supplemented with the antibiotic required to maintain the antisense construct and are diluted 1:100 in identical medium immediately prior to addition to the microtiter plate wells. For a control, cells are also added to several wells that lack antibiotic, but contain the solvent used to dissolve the antibiotics. Cell growth is monitored continuously by incubation at 37°C in a microtiter plate reader monitoring the OD_{600} of the wells over an 18-hour period. The percent inhibition of growth produced by each concentration of antibiotic is calculated by comparing the rates of logarithmic growth against that exhibited by cells growing in medium without antibiotic. A plot of percent inhibition against log[antibiotic concentration] allows extrapolation of an IC_{50} value for each antibiotic.

E. Measurement of Test Antibiotic Sensitivity in the Presence of Antisense Construct Inducer

The culture medium selected for use in the assay is supplemented with inducer at concentrations shown to inhibit cell growth by 50% and 80% as described above, as well as the antibiotic used to maintain the construct. Two-fold dilution series of the panel of test antibiotics used above are generated in each of these media. Several antibiotics are tested side by side in each medium with three to four wells being used to evaluate the effects of an antibiotic on cell growth at each concentration. Equal volumes of test antibiotic and cells are added to the wells of a 384 well

microtiter plate and mixed. Cells are prepared as described above using the medium selected for use in the assay supplemented with the antibiotic required to maintain the antisense construct. The cells are diluted 1:100 into two 50 mL aliquots of identical medium containing concentrations of inducer that have been shown to inhibit cell growth by 50% and 80 % respectively and incubated at 37°C with shaking for 2.5 hours. Immediately prior to addition to the microtiter plate wells, the cultures are adjusted to an appropriate OD_{600} (typically 0.002) by dilution into warm (37°C) sterile medium supplemented with identical concentrations of the inducer and antibiotic used to maintain the antisense construct. For a control, cells are also added to several wells that contain solvent used to dissolve test antibiotics but which contain no antibiotic. Cell growth is monitored continuously by incubation at 37°C in a microtiter plate reader monitoring the OD_{600} of the wells over an 18-hour period. The percent inhibition of growth produced by each concentration of antibiotic is calculated by comparing the rates of logarithmic growth against that exhibited by cells growing in medium without antibiotic. A plot of percent inhibition against log[antibiotic concentration] allows extrapolation of an IC_{50} value for each antibiotic.

F. Determining the Specificity of the Test Antibiotics

A comparison of the IC_{50}s generated by antibiotics of known mechanism of action under antisense induced and non-induced conditions allows the pathway in which a proliferation-required nucleic acid lies to be identified. If cells expressing an antisense nucleic acid comprising a nucleotide sequence complementary to a proliferation-required gene are selectively sensitive to an antibiotic acting via a particular pathway, then the gene against which the antisense acts is involved in the pathway on which the antibiotic acts.

G. Identification of Pathway in which a Test Antibiotic Acts

As discussed above, the cell-based assay may also be used to determine the pathway against which a test antibiotic acts. In such an analysis, the pathways against which each member of a panel of antisense nucleic acids acts are identified as described above. A panel of cells, each containing an inducible vector which transcribes an antisense nucleic acid comprising a nucleotide sequence complementary to a gene in a known proliferation-required pathway, is contacted with a test antibiotic for which it is desired to determine the pathway on which it acts under inducing and non-inducing conditions. If heightened sensitivity is observed in induced cells transcribing antisense complementary to a gene in a particular pathway but not in induced cells transcribing antisense nucleic acids comprising nucleotide sequences complementary to genes in other pathways, then the test antibiotic acts against the pathway for which heightened sensitivity was observed.

One skilled in the art will appreciate that further optimization of the assay conditions, such as the concentration of inducer used to induce antisense transcription and/or the growth conditions used for the assay (for example incubation temperature and medium components) may further increase the selectivity and/or magnitude of the antibiotic sensitization exhibited.

It will be appreciated that the above cell-based assays may be performed using antisense nucleic acids comprising nucleotide sequences complementary to any of the proliferation-required nucleic acids from *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae* or *Yersinia pestis* (including antisense nucleic acids comprising nucleotide sequences complemenatary to SEQ ID NOs: 6214-42397, such as the antisense nucleic acids of SEQ ID NOs.: 1-6213) or portions thereof, antisense nucleic acids complementary to homologous coding nucleic acids or portions thereof, or homologous antisense nucleic acids. In this way, the level or activity of a target, such as any of the proliferation-required polypeptides from *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae* or *Yersinia pestis* (including the polypeptides of SEQ ID NOs.: 42398-78581), or homologous polypeptides may be reduced.

In some embodiments of the present invention, the methods for the production of stabilized RNA, as described in U.S. Provisional Patent Application Serial Number 60/343,512, can be used in the above cell-based assays in Gram-negative organisms to extend the lifetime of transcripts corresponding to the nucleic acids described herein.

The following example confirms the effectiveness of the methods described above.

EXAMPLE 19

Identification of the Biological Pathway in which a Proliferation-Required Gene Lies

The effectiveness of the above assays was validated using proliferation-required genes from *E. coli* which were identified using procedures similar to those described above. Antibiotics of various chemical classes and modes of action were purchased from Sigma Chemicals (St. Louis, MO). Stock solutions were prepared by dissolving each antibiotic in an appropriate aqueous solution based on information provided by the manufacturer. The final working solution of each antibiotic contained no more than 0.2% (w/v) of any organic solvent. To determine their potency against a bacterial strain engineered for transcription of an antisense comprising a nucleotide sequence complementary to a proliferation-required 50S ribosomal protein, each antibiotic was serially diluted two- or three- fold in growth medium supplemented with the appropriate antibiotic for maintenance of the antisense construct. At least ten dilutions were prepared for each antibiotic. 25 μL aliquots of each dilution were transferred to discrete wells of a 384-well microplate (the assay plate) using a multi-channel pipette. Quadruplicate wells were used for each dilution of an antibiotic under each treatment condition (plus and minus inducer). Each assay plate contained twenty wells for cell growth controls (growth medium replacing antibiotic), ten wells for each treatment (plus and minus inducer, in this example IPTG). Assay plates were usually divided into the two treatments: half the plate containing induced cells and an appropriate concentrations of inducer (in this example IPTG) to maintain the state of induction, the other half containing non-induced cells in the absence of IPTG.

Cells for the assay were prepared as follows. Bacterial cells containing a construct, from which transcription of antisense nucleic acid comprising a nucleotide sequence complementary to *rplL* and *rplJ (*AS-*rplL/J)*, which encode proliferation-required 50S ribosomal subunit proteins, is inducible in the presence of IPTG, were grown into exponential growth (OD_{600} 0.2 to 0.3) and then diluted 1:100 into fresh medium containing either 400 μM or 0 μM inducer (IPTG). These cultures were incubated at 37° C for 2.5 hr. After a 2.5 hr incubation, induced and non-induced cells were respectively diluted into an assay medium at a final OD_{600} value of 0.0004. The medium contained an appropriate concentration of the antibiotic for the maintenance of the antisense construct. In addition, the medium used to dilute induced cells was supplemented with 800 μM IPTG so that addition to the assay plate would result in a final IPTG concentration of 400 μM. Induced and non-induced cell suspensions were dispensed (25 μl/well) into the appropriate wells of the assay plate as discussed previously. The plate was then loaded into a plate reader, incubated at constant temperature, and cell growth was monitored in each well by the measurement of light scattering at 595 nm. Growth was monitored every 5 minutes until the cell culture attained a stationary growth phase. For each concentration of antibiotic, a percentage inhibition of growth was calculated at the time point corresponding to mid-exponential growth for the associated control wells (no antibiotic, plus or minus IPTG). For each antibiotic or minus IPTG), a plot of percent

inhibition versus log of antibiotic concentration was generated and the IC_{50} determined. A comparison of the IC_{50} for each antibiotic in the presence and absence of IPTG revealed whether induction of the antisense construct sensitized the cell to the mechanism of action exhibited by the antibiotic. Cells which exhibited a statistically significant decrease in the IC_{50} value in the presence of inducer were considered to have an increased sensitivity to the test antibiotic.

The results are provided in the table below, which lists the classes and names of the antibiotics used in the analysis, the targets of the antibiotics, the IC_{50} in the absence of IPTG, the IC_{50} in the presence of IPTG, the concentration units for the IC_{50s}, the fold increase in IC_{50} in the presence of IPTG, and whether increased sensitivity was observed in the presence of IPTG.

TABLE V

Effect of Expression of Antisense RNA to *rplL* and *rplJ* on Antibiotic Sensitivity

ANTIBIOTIC CLASS /Names	TARGET	IC_{50} (-IPTG)	IC_{50} (+IPTG)	Conc. Unit	Fold Increase in Sensitivity	Sensitivity Increased?
PROTEIN SYNTHESIS INHIBITOR						
AMINOGLYCOSIDES						
Gentamicin	30S ribosome function	2715	19.19	ng/ml	141	Yes
Streptomycin	30S ribosome function	11280	161	ng/ml	70	Yes
Spectinomycin	30S ribosome function	18050	<156	ng/ml		Yes
Tobramycin	30S ribosome function	3594	70.58	ng/ml	51	Yes
MACROLIDES						
Erythromycin	50S ribosome function	7467	187	ng/ml	40	Yes
AROMATIC POYKETIDES						
Tetracycline	30S ribosome function	199.7	1.83	ng/ml	109	Yes
Minocycline	30S ribosome function	668.4	3.897	ng/ml	172	Yes
Doxycycline	30S ribosome function	413.1	27.81	ng/ml	15	Yes
OTHER PROTEIN SYNTHESIS INHIBITORS						
Fusidic acid	Elongation Factor G function	59990	641	ng/ml	94	Yes
Chloramphenicol	30S ribosome function	465.4	1.516	ng/ml	307	Yes
Lincomycin	50S ribosome function	47150	324.2	ng/ml	145	Yes
OTHER ANTIBIOTIC MECHANISMS						
B-LACTAMS						
Cefoxitin	Cell wall biosynthesis	2782	2484	ng/ml	1	No
Cefotaxime	Cell wall biosynthesis	24.3	24.16	ng/ml	1	No
DNA SYNTHESIS INHIBITORS						
Nalidixic acid	DNA Gyrase activity	6973	6025	ng/ml	1	No
Ofloxacin	DNA Gyrase activity	49.61	45.89	ng/ml	1	No
OTHER						
Bacitracin	Cell membrane function	4077	4677	mg/ml	1	No
Trimethoprim	Dihydrofolate Reductase activity	128.9	181.97	ng/ml	1	No
Vancomycin	Cell wall biosynthesis	145400	72550	ng/ml	2	No

The above results demonstrate that induction of an antisense RNA complementary to genes encoding 50S ribosomal subunit proteins results in a selective and highly significant sensitization of cells to antibiotics that inhibit ribosomal function and protein synthesis. The above results further demonstrate that induction of an antisense to an essential gene sensitizes a cell or microorganism to compounds that interfere with that gene product's biological role. This sensitization is restricted to compounds that interfere with pathways associated with the targeted gene and its product.

It will be appreciated that the above cell-based assays may be performed using antisense nucleic acids complementary to any of the proliferation-required nucleic acids from *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae* or *Yersinia pestis* (including antisense nucleic acids complementary to SEQ ID NOs. 6214-42397, such as the antisense nucleic acids of SEQ ID NOs.: 1-6213) or portions thereof, antisense nucleic acids complementary to homologous coding nucleic acids or portions thereof or homologous antisense nucleic acids. In this way, the level or activity of a target, such as any of the proliferation-required polypeptides from *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis,*

Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae or *Yersinia pestis* (including the polypeptides of SEQ ID NOs.: 42398-78581), or homologous polypeptides may be reduced.

In some embodiments of the present invention, the methods for the production of stabilized RNA, as described in U.S. Provisional Patent Application Serial Number 60/343,512, can be used in the above cell-based assays in Gram-negative organisms to extend the lifetime of transcripts corresponding to the nucleic acids described herein.

Example 20 below describes an analysis performed in *Staphylococcus aureus*.

EXAMPLE 20

Identification of the Biological Pathway in which a Gene Required for Proliferation of *Staphylococcus aureus* Lies

Antibiotics of various chemical classes and modes of action were purchased from chemical suppliers, for example Sigma Chemicals (St. Louis, MO). Stock solutions were prepared by dissolving each antibiotic in an appropriate aqueous solution based on information provided by the manufacturer. The final working solution of each antibiotic contained no more than 0.2% (w/v) of any organic solvent.

To determine its potency against a bacterial strain containing an antisense nucleic acid comprising a nucleotide sequence complementary to the nucleotide sequence encoding the Beta subunit of DNA gyrase (which is required for proliferation) under the control of a xylose inducible promoter, each antibiotic was serially diluted two- or three- fold in growth medium supplemented with the appropriate antibiotic for maintenance of the antisense construct. At least ten dilutions were prepared for each antibiotic.

Aliquots (25 μL) of each dilution were transferred to discrete wells of a 384-well microplate (the assay plate) using a multi-channel pipette. Quadruplicate wells were used for each dilution of an antibiotic under each treatment condition (plus and minus inducer). Each assay plate contained twenty wells for cell growth controls (growth medium, no antibiotic), ten wells for each treatment (plus and minus inducer, xylose, in this example). Half the assay plate contained induced cells (in this example *Staphylococcus aureus* cells) and appropriate concentrations of inducer (xylose, in this example) to maintain the state of induction while the other half of the assay plate contained non-induced cells maintained in the absence of inducer.

Preparation of Bacterial Cells

Cells of a bacterial clone containing a construct in which transcription of antisense comprising a nucleotide sequence complementary to the sequence encoding the Beta subunit of DNA gyrase under the control of the xylose inducible promoter (S1M10000001F08) were grown into exponential growth (OD_{600} 0.2 to 0.3) and then diluted 1:100 into fresh medium containing either 12 mM or 0 mM inducer (xylose). These cultures were incubated at 37° C for 2.5 hr. The presence of inducer (xylose) in the medium initiates and maintains production of antisense RNA from the antisense construct. After a 2.5 hr incubation, induced and non-induced cells were respectively diluted into an assay medium containing an appropriate concentration of the antibiotic for the maintenance of the antisense construct. In addition, medium used to dilute induced cells was supplemented with 24 mM xylose so that addition to the assay plate would result in a final xylose concentration of 12 mM. The cells were diluted to a final OD_{600} value of 0.0004.

Induced and non-induced cell suspensions were dispensed (25 µl/well) into the appropriate wells of the assay plate as discussed previously. The plate was then loaded into a plate reader and incubated at constant temperature while cell growth was monitored in each well by the measurement of light scattering at 595 nm. Growth was monitored every 5 minutes until the cell culture attained a stationary growth phase. For each concentration of antibiotic, a percentage inhibition of growth was calculated at the time point corresponding to mid-exponential growth for the associated control wells (no antibiotic, plus or minus xylose). For each antibiotic and condition (plus or minus xylose), plots of percent inhibition versus Log of antibiotic concentration were generated and IC_{50s} determined.

A comparison of each antibiotic's IC_{50} in the presence and absence of inducer (xylose, in this example) reveals whether induction of the antisense construct sensitized the cell to the antibiotic's mechanism of action. If the antibiotic acts against the β subunit of DNA gyrase, the IC_{50} of induced cells will be significantly lower than the IC_{50} of uninduced cells.

Figure 10 lists the antibiotics tested, their targets, and their fold increase in potency between induced cells and uninduced cells. As illustrated in Figure 10, the potency of cefotaxime, cefoxitin, fusidic acid, lincomycin, tobramycin, trimethoprim and vancomycin, each of which act on targets other than the β subunit of gyrase, was not significantly different in induced cells as compared to uninduced cells. However, the potency of novobiocin, which is known to act against the Beta subunit of DNA gyrase, was significantly different between induced cells and uninduced cells.

Thus, induction of an antisense nucleic acid comprising a nucleotide sequence complementary to the sequence encoding the β subunit of gyrase results in a selective and

significant sensitization of *Staphylococcus aureus* cells to an antibiotic which inhibits the activity of this protein. Furthermore, the results demonstrate that induction of an antisense construct to an essential gene sensitizes a cell or microorganism to compounds that interfere with that gene product's biological role. This sensitization is apparently restricted to compounds that interfere with the targeted gene and its product.

It will be appreciated that the above cell-based assays may be performed using antisense nucleic acids complementary to any of the proliferation-required nucleic acids from *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae* or *Yersinia pestis* (including antisense nucleic acids complementary to SEQ ID NOs.: 6214-42397, such as the antisense nucleic acids of SEQ ID NOs. 1-6213), or portions thereof, antisense nucleic acids complementary to homologous coding nucleic acids or portions thereof, or homologous antisense nucleic acids. In this way, the level or activity of a target, such as any of the proliferation-required polypeptides from *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus*

mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae or *Yersinia pestis* or homologous polypeptides may be reduced.

In some embodiments of the present invention, the methods for the production of stabilized RNA, as described in U.S. Provisional Patent Application Serial Number 60/343,512, can be used in the above cell-based assays in Gram-negative organisms to extend the lifetime of transcripts corresponding to the nucleic acids described herein.

Assays utilizing antisense constructs to essential genes or portions thereof can be used to identify compounds that interfere with the activity of those gene products. Such assays could be used to identify drug leads, for example antibiotics.

Panels of cells transcribing different antisense nucleic acids can be used to characterize the point of intervention of a compound affecting an essential biochemical pathway including antibiotics with no known mechanism of action.

Assays utilizing antisense constructs to essential genes can be used to identify compounds that specifically interfere with the activity of multiple targets in a pathway. Such constructs can be used to simultaneously screen a sample against multiple targets in one pathway in one reaction (Combinatorial HTS).

Furthermore, as discussed above, panels of antisense construct-containing cells may be used to characterize the point of intervention of any compound affecting an essential biological pathway including antibiotics with no known mechanism of action.

It will be appreciated that the above cell-based assays may be performed using antisense nucleic acids complementary to any of the proliferation-required nucleic acids from *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans,*

Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae or *Yersinia pestis* (including antisense nucleic acids comprising nucleotide sequences complementary to SEQ ID NOs.: 6214-42397, such as the antisense nucleic acids of SEQ ID NOs. 1-6213), or portions thereof, antisense nucleic acids complementary to homologous coding nucleic acids or portions thereof, or homologous antisense nucleic acids. In this way, the level or activity of a target, such as any of the proliferation-required polypeptides from *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae* or *Yersinia pestis* or homologous polypeptides may be reduced.

In some embodiments of the present invention, the methods for the production of stabilized RNA, as described in U.S. Provisional Patent Application Serial Number 60/343,512, can be used in the above cell-based assays in Gram-negative organisms to extend the lifetime of transcripts corresponding to the nucleic acids described herein.

Another embodiment of the present invention is a method for determining the pathway against which a test antibiotic compound is active, in which the activity of target proteins or nucleic acids involved in proliferation-required pathways is reduced by contacting cells with a sub-lethal concentration of a known antibiotic which acts against the target protein or nucleic acid. In one embodiment, the target protein or nucleic acid corresponds to a proliferation-required nucleic acid identified using the methods described above, such as the polypeptides of SEQ ID NOs.: 42398-78581, or homologous polypeptides. The method is similar to those described above for determining which pathway a test antibiotic acts against, except that rather than reducing the activity or level of a proliferation-required gene product using a sub-lethal level of antisense to a proliferation-required nucleic acid, the sensitized cell is generated by

reducing the activity or level of the proliferation-required gene product using a sub-lethal level of a known antibiotic which acts against the proliferation required gene product. Heightened sensitivity determines the pathway on which the test compound is active.

Interactions between drugs which affect the same biological pathway have been described in the literature. For example, Mecillinam (Amdinocillin) binds to and inactivates the penicillin binding protein 2 (PBP2, product of the *mrdA* in *E. coli*). This antibiotic interacts with other antibiotics that inhibit PBP2 as well as antibiotics that inhibit other penicillin binding proteins such as PBP3 [(Gutmann, L., Vincent, S., Billot-Klein, D., Acar, J.F., Mrena, E., and Williamson, R. (1986) Involvement of penicillin-binding protein 2 with other penicillin-binding proteins in lysis of *Escherichia coli* by some beta-lactam antibiotics alone and in synergistic lytic effect of amdinocillin (mecillinam). Antimicrobial Agents & Chemotherapy, 30:906-912). Interactions between drugs could, therefore, involve two drugs that inhibit the same target protein or nucleic acid or inhibit different proteins or nucleic acids in the same pathway [(Fukuoka, T., Domon, H., Kakuta, M., Ishii, C., Hirasawa, A., Utsui, Y., Ohya, S., and Yasuda, H. (1997) Combination effect between panipenem and vancomycin on highly methicillin-resistant *Staphylococcus aureus*. Japan. J. Antibio. 50:411-419; Smith, C.E., Foleno, B.E., Barrett, J.F., and Frosc, M.B. (1997) Assessment of the synergistic interactions of levofloxacin and ampicillin against *Enterococcus faecium* by the checkerboard agar dilution and time-kill methods. Diagnos. Microbiol. Infect. Disease 27:85-92; den Hollander, J.G., Horrevorts, A.M., van Goor, M.L., Verbrugh, H.A., and Mouton, J.W. (1997) Synergism between tobramycin and ceftazidime against a resistant *Pseudomonas aeruginosa* strain, tested in an in vitro pharmacokinetic model. Antimicrobial Agents & Chemotherapy. 41:95-110).

Two drugs may interact even though they inhibit different targets. For example, the proton pump inhibitor, Omeprazole, and the antibiotic, Amoxycillin, two synergistic compounds acting together, can cure *Helicobacter pylori* infection [(Gabryelewicz, A., Laszewicz, W., Dzieniszewski, J., Ciok, J., Marlicz, K., Bielecki, D., Popiela, T., Legutko, J., Knapik, Z., Poniewierka, E. (1997) Multicenter evaluation of dual-therapy (omeprazol and amoxycillin) for *Helicobacter pylori*-associated duodenal and gastric ulcer (two years of the observation). J. Physiol. Pharmacol. 48 Suppl 4:93-105).

The growth inhibition from the sub-lethal concentration of the known antibiotic may be at least about 5%, at least about 8%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, or at least about 75%, or more.

Alternatively, the sub-lethal concentration of the known antibiotic may be determined by measuring the activity of the target proliferation-required gene product rather than by measuring growth inhibition.

Cells are contacted with a combination of each member of a panel of known antibiotics at a sub-lethal level and varying concentrations of the test antibiotic. As a control, the cells are contacted with varying concentrations of the test antibiotic alone. The IC_{50} of the test antibiotic in the presence and absence of the known antibiotic is determined. If the IC_{50}s in the presence and absence of the known drug are substantially similar, then the test drug and the known drug act on different pathways. If the IC_{50}s are substantially different, then the test drug and the known drug act on the same pathway.

It will be appreciated that the above cell-based assays may be performed using a sub-lethal concentration of a known antibiotic which acts against the product of any of the proliferation-required nucleic acids from *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae* or *Yersinia pestis* (including the products of SEQ ID NOs: 6214-42397, or portions thereof, or the products of homologous coding nucleic acids or portions thereof. In this way, the level or activity of a target, such as any of the proliferation-required polypeptides from *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria*

meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae or *Yersinia pestis* (including the polypeptides of SEQ ID NOs.: 42398-78581), or homologous polypeptides may be reduced.

Another embodiment of the present invention is a method for identifying a candidate compound for use as an antibiotic in which the activity of target proteins or nucleic acids involved in proliferation-required pathways is reduced by contacting cells with a sub-lethal concentration of a known antibiotic which acts against the target protein or nucleic acid. In one embodiment, the target protein or nucleic acid is a target protein or nucleic acid corresponding to a proliferation-required nucleic acid identified using the methods described above. The method is similar to those described previously herein for identifying candidate compounds for use as antibiotics except that rather than reducing the activity or level of a proliferation-required gene product using a sub-lethal level of antisense to a proliferation-required nucleic acid, the activity or level of the proliferation-required gene product is reduced using a sub-lethal level of a known antibiotic which acts against the proliferation required gene product.

The growth inhibition from the sub-lethal concentration of the known antibiotic may be at least about 5%, at least about 8%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, or at least about 75%, or more.

Alternatively, the sub-lethal concentration of the known antibiotic may be determined by measuring the activity of the target proliferation-required gene product rather than by measuring growth inhibition.

In order to characterize test compounds of interest, cells are contacted with a panel of known antibiotics at a sub-lethal level and one or more concentrations of the test compound. As a control, the cells are contacted with the same concentrations of the test compound alone. The IC_{50} of the test compound in the presence and absence of the known antibiotic is determined. If the IC_{50} of the test compound is substantially different in the presence and absence of the known drug then the test compound is a good candidate for use as an antibiotic. As discussed above, once a candidate compound is identified using the above methods its structure may be optimized using standard techniques such as combinatorial chemistry.

Representative known antibiotics which may be used in each of the above methods are provided in Table VI below. However, it will be appreciated that other antibiotics may also be used.

TABLE VI
Antibiotics and Their Targets

ANTIBIOTIC	INHIBITS/TARGET	RESISTANT MUTANTS
Inhibitors of Transcription		
Rifamycin, Rifampicin Rifabutin Rifaximin	Inhibits initiation of transcription/ß-subunit RNA polymerase, *rpoB*	*rpoB, crp, cyaA*
Streptolydigin	Accelerates transcription chain termination/ß-subunit RNA polymerase	*rpoB*
Streptovaricin	an acyclic ansamycin, inhibits RNA polymerase	*rpoB*
Actinomycin D+EDTA	Intercalates between 2 successive G-C pairs, *rpoB,* inhibits RNA synthesis	*pldA*
Inhibitors of Nucleic Acid Metabolism		
Quinolones, Nalidixic acid Oxolinic acid	α subunit gyrase and/or topoisomerase IV, *gyrA*	*gyrAorB, icd, sloB*
Fluoroquinolones Ciprofloxacin, Norfloxacin	α subunit gyrase, *gyrA* and/or topoisomerase IV (probable target in Staph)	*gyrA* *norA* (efflux in Staph) *hipQ*
Coumerins Novobiocin	Inhibits ATPase activity of ß-subunit gyrase, *gyrB*	*gyrB, cysB, cysE, nov, ompA*
Coumermycin	Inhibits ATPase activity of ß-subunit gyrase, *gyrB*	*gyrB, hisW*
Albicidin	DNA synthesis	*tsx* (nucleoside channel)
Metronidazole	Causes single-strand breaks in DNA	*nar*
Inhibitors of Metabolic Pathways		
Sulfonamides, Sulfanilamide	blocks synthesis of dihydrofolate,dihydro-pteroate synthesis, *folP*	*folP, gpt, pabA, pabB, pabC*
Trimethoprim,	Inhibits dihydrofolate reductase, *folA*	*folA, thyA*
Showdomycin	Nucleoside analogue capable of alkylating sulfhydryl groups, inhibitor of thymidylate synthetase	*nupC, pnp*
Thiolactomycin	type II fatty acid synthase inhibitor	*emrB* *fadB, emrB* due to gene dosage
Psicofuranine	Adenosine glycoside antibiotic, target is GMP synthetase	*guaA,B*
Triclosan	Inhibits fatty acid synthesis	*fabI (envM)*
Diazoborines Isoniazid, Ethionamide	heterocyclic, contain boron, inhibit fatty acid synthesis, enoyl-ACP reductase, *fabI*	*fabI (envM)*

Inhibitors of Translation		
Phenylpropanoids Chloramphenicol,	Binds to ribosomal peptidyl transfer center preventing peptide translocation/ binds to S6, L3, L6, L14, L16, L25, L26, L27, but preferentially to L16	*rrn, cmlA, marA, ompF, ompR*
Tetracyclines, type II polyketides Minocycline Doxycycline	Binding to 30S ribosomal subunit, "A" sit on 30S subunit, blocks peptide elongation, strongest binding to S7	*clmA (cmr), mar, ompF*
Macrolides (type I polyketides) Erythromycin, Carbomycin, Spiramycin etc	Binding to 50 S ribosomal subunit, 23S rRNA, blocks peptide translocation, L15, L4, L12	*rrn, rplC, rplD, rplV , mac*
Aminoglycosides Streptomycin, Neomycin Spectinomycin Kanamycin Kasugamycin Gentamicin, Amikacin Paromycin	Irreversible binding to 30S ribosomal subunit, prevents translation or causes mistranslation of mRNA/16S rRNA	*rpsL, strC,M, ubiF* *atpA-E, ecfB, hemAC,D,E,G, topA,* *rpsC,D,E, rrn, spcB* *atpA-atpE, cpxA, ecfB, hemA,B,L, topA* *ksgA,B,C,D, rplB,K, rpsI,N,M,R* *rplF, ubiF* *cpxA* *rpsL*
Lincosamides Lincomycin, Clindamycin	Binding to 50 S ribosomal subunit, blocks peptide translocation	*linB, rplN,O, rpsG*
Streptogramins Virginiamycin, Pristinamycin Synercid: quinupristin /dalfopristin	2 components, Streptogramins A&B, bind to the 50S ribosomal subunit blocking peptide translocation and peptide bond formation	
Fusidanes Fusidic Acid	Inhibition of elongation factor G (EF-G) prevents peptide translocation	*fusA*
Kirromycin (Mocimycin)	Inhibition of elongation factor TU (EF-Tu), prevents peptide bond formation	*tufA,B*
Pulvomycin	Binds to and inhibits EF-TU	
Thiopeptin	Sulfur-containing antibiotic, inhibits protein synthesis,EF-G	*rplE*
Tiamulin	Inhibits protein synthesis	*rplC, rplD*
Negamycin	Inhibits termination process of protein synthesis	*prfB*
Oxazolidinones Linezolid Isoniazid	23S rRNA	*pdx*
Nitrofurantoin	Inhibits protein synthesis,	*nfnA,B*

	nitroreductases convert nitrofurantoin to highly reactive electrophilic intermediates which attack bacterial ribosomal proteins non-specifically	
Pseudomonic Acids Mupirocin (Bactroban)	Inhibition of isoleucyl tRNA synthetase-used for Staph, topical cream, nasal spray	*ileS*
Indolmycin	Inhibits tryptophanyl-tRNA synthetase	*trpS*
Viomycin		*rrmA* (23S rRNA methyltransferase; mutant has slow growth rate, slow chain elongation rate, and viomycin resistance)
Thiopeptides	Binds to L11-23S RNA complex	
Thiostrepton	Inhibits GTP hydrolysis by EF-G	
Micrococcin	Stimulates GTP hydrolysis by EF-G	

Inhibitors of Cell Walls/Membranes

ß-lactams	Inhibition of one or more cell wall transpeptidases, endopeptidases, and glycosidases (PBPs), of the 12 PBPs only 2 are essential: *mrdA* (PBP2) and *ftsI (pbpB,* PBP3)	
Penicillin, Ampicillin Methicillin,		*ampC, ampD, ampE, envZ, galU, hipA, hipQ, ompC, ompF, ompR, ptsI, rfa, tolD, tolE*
Cephalosporins,		*tonB*
Mecillinam (amdinocillin)	Binds to and inactivates PBP2 (*mrdA*) Inactivates PBP3 (*ftsI*)	*alaS, argS, crp, cyaA, envB, mrdA,B, mreB,C,D*
Aztreonam (Furazlocillin)		
Bacilysin, Tetaine	Dipeptide, inhib glucosamine synthase	*dppA*
Glycopeptides Vancomycin,	Inhib G+ cell wall syn, binds to terminal D-ala-D-ala of pentapeptide,	
Polypeptides Bacitracin	Prevents dephosphorylation and regeneration of lipid carrier	*rfa*
Cyclic lipopeptide Daptomycin,	Disrupts multiple aspects of membrane function, including peptidoglycan synthesis, lipoteichoic acid synthesis, and the bacterial membrane potential	
Cyclic polypeptides Polymixin,	Surfactant action disrupts cell membrane lipids, binds lipid A mioety of LPS	*pmrA*
Fosfomycin,	Analogue of P-enolpyruvate, inhibits 1st step in peptidoglycan synthesis - UDP-N-acetylglucosamine	*murA, crp, cyaA glpT, hipA, ptsI, uhpT*

	enolpyruvyl transferase, *murA*. Also acts as Immunosuppressant	
Cycloserine	Prevents formation of D-ala dimer, inhibits D-ala ligase, *ddlA,B*	*hipA, cycA*
Alafosfalin	phosphonodipeptide, cell wall synthesis inhibitor, potentiator of ß-lactams	*pepA, tpp*

Inhibitors of Protein Processing/Transport

Globomycin	Inhibits signal peptidase II (cleaves prolipoproteins subsequent to lipid modification, *lspA*	*lpp, dnaE*

It will be appreciated that the above cell-based assays may be performed using a sub-lethal concentration of a known antibiotic which acts against the product of any of the proliferation-required nucleic acids from *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae* or *Yersinia pestis* or portions thereof, or homologous nucleic acids. In this way, the level or activity of a target, such as any of the proliferation-required polypeptides from *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria*

meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae or *Yersinia pestis* or homologous polypeptides may be reduced.

EXAMPLE 21

Strains in which a Gene Encoding a Gene Product Required for Proliferation is Overexpressed are able to Grow at Elevated Antibiotic Concentrations

To confirm that cells which overexpress a gene product required for proliferation are able to grow at elevated antibiotic concentrations, 11 such genes from *Staphylococcus aureus* which are the targets of known antibiotics were operably linked to the xylose inducible promoter XylT5 (described in U.S. Patent Application Serial Number 10/032,393. The genes and the antibiotics which target the products of these genes are listed in Table VII below.

PCR primer pairs were designed for each of the 11 genes encoding a gene product required for proliferation of *Staphylococcus aureus* as shown in Table VII. The upstream primers for each gene included the native ribosomal binding sites (S-D sequences). In addition, restriction sites for appropriate restriction enzymes were designed into the primers to facilitate directional cloning of the genes. PCR reactions were carried out using Pfu DNA polymerase (Stratagene, San Diego) under the following conditions per 50 µl reaction: Pfu polymerase 2U, dNTP 200 µM, primers 400 nM each, *S. aureus* RN450 genomic DNA (template) 5-10 ng. The reaction involved an initial heating at 94°C for 5 min, followed by 25 cycles of 30 sec at 94°C/30 sec at 55°C/5 min at 72°C, and ending with 7 min of extension at 72°C.

The amplified genes were operably linked to the XylT5 promoter as follows. PCR products were cleaned using QIAGEN PCR Cleaning Kits and then were digested with the proper restriction enzymes. The resulting fragments were ligated overnight at 16°C with precut vector DNA containing the XylT5 promoter. Ligation mixtures were ethanol precipitated at -80°C for 20 min in the presence of 0.3 M sodium acetate. The precipitated DNA was spun down at 14,000 rpm for 30 min at 4°C and washed with 1 ml of 70% EtoH. The DNA pellets were air-dried and dissolved in EB or sterile water. To transform *Staphylococcus aureus* cells, the precipitated DNA was mixed with 45 µl of electroporation competent cells and incubated at room temperature for 30 min. The DNA/cell mixtures were electroporated (settings: 2 volts, 25 µF, 200 Ω) in 2 mm cuvettes and mixed with 450 µl B2 medium containing 0.2 µg/ml chloramphenicol. The cells were incubated at 37°C with shaking for 90 min. Transformed cells were plated onto LB agar plates containing chloramphenicol (34 µg/ml) for the selection of plasmids. Several colonies for each cloning reaction were picked and streaked to obtain a pure

culture. Colony PCR reactions using vector-specific primers were performed to verify the size and identity of the inserts.

Gene-walking sequencing was employed to completely sequence the entire insert for several clones of each cloned gene. This was carried out to avoid using a cloned gene whose DNA sequence was mutated during the PCR process.

To demonstrate that genes encoding gene products required for proliferation can confer resistance to their specific inhibitors upon induction at proper inducer levels, cells of each clone in which the genes were operably linked to the xylose inducible promoter were grown in LB medium with chloramphenicol (34 μg/ml) at a combination of differing antibiotic and inducer concentrations. This was accomplished by using microtitration plates (96 or 384 wells) which contained antibiotic and inducer at gradient concentrations in a matrix format in 10 times excess quantity (see Figure 11). Media containing inoculated cells (9 volume) was dispensed into the wells containing 1 volume of antibiotic/inducer for a final volume of 50 μl (for 384 well plates) or 200 μl (for 96 well plates). The plates were incubated at 37°C with periodic shaking and growth of cells was monitored by automatic measurement of optical density at OD600 using a Ultramark reader. A clone over-expressing a particular gene was considered resistant to its specific antibiotic (inhibitor) if significant growth was observed at appropriate inducer concentrations in the presence of a particular concentration of antibiotic but not in the absence of inducer at that concentration of antibiotic.

The results are indicated in Figure 12 and Figure 13. As illustrated in Figure 12, at appropriate concentrations of inducer cells which overexpress the *defB* gene product were able to grow at elevated concentrations of the antibiotic actinonin, which acts on the *defB* gene product. Similarly, as illustrated in Figure 13, at appropriate concentrations of inducer cells which overexpress the *folA* gene product were able to grow at elevated concentrations of the antibiotic trimethoprim, which acts on the folA gene product.

Thus, elevated expression of a gene product required for proliferation enables cells to grow in the presence of antibiotic concentrations which inhibit or prevent growth of wild type cells.

Table VII - Essential Genes/Proteins and Specific Inhibitors

Gene	Target	Inhibitor	Primers
gyrB	β subunit of DNA gyrase or topoisomerase II	Novobiocin	GCCGGATCCTTATAAAGTAACAGAAAGCGATGGTGACTGC (SEQ ID NO. : 78593); CAGGTCGACCAGCGCTTAGAAGTCTAAGTTTGCATAAACTG (SEQ ID NO.: 78594)
murA	UDP-N-acetylglucosamine enolpyruvyl transferase	Fosfomycin	CCTGGATCCTTCTAAGTGGAGGATTTACG (SEQ ID NO.: 78595); CAGGTCGACGAATTAATCGTTAATACGTT (SEQ ID NO.: 78596)
fabI	Enoyl-acyl carrier protein reductase	Triclosan	GCCGGATCCATAAGGAGTTATCTTACATG (SEQ ID NO.: 78597); CGCGTCGACTTATTTAATTGCGTGGAATC (SEQ ID NO.: 78598)
rpoB	RNA polymerase β subunit	Rifampicin	GCTGGATCCTGAGGGGTGAATCTGTTTGGC (SEQ ID NO.: 78599); CTGCTCGAGTGCGTATTAATCAGTAACTT (SEQ ID NO.: 78600)
fusA	Elongation factor G	Fusidic acid	GCTGGATCCCTGGAAGGAGAAAAAATACATGGCTAGAG (SEQ ID NO.: 78601); CCGGTCGACGGCTAGCTAGTCAAAACAAGTTATATTATTCAC (SEQ ID NO.: 78602)
folA	Dihydrofolate reductase	Trimethoprim	GCTGGATCCAGAAGAAGGAGGATAATTATG (SEQ ID NO.: 78603); CCGGTCGACTTTTCCCCCTTATTTTTTAC (SEQ ID NO.: 78604)
ileS	Isoleucyl tRNA synthetase	Mupirocin (bactroban)*	GCTGGATCCTAAGGAGTGAAAAAAATGGATTACAAAGAAACG (SEQ ID NO.: 78605); CCGGTCGACCAATTATACAAGTGATTTTACAACTTGTTGGCATC (SEQ ID NO.: 78606)
trpS	Tryptophanyl tRNA synthetase	Indolmycin*	GCGGGATCCCTAAGAAAGTAGGCATTTAAATGGAGAC (SEQ ID NO.: 78607); CCGGTCGACGTTTATTTTATCTCTTACGTCCTAAACC (SEQ ID NO.: 78608)
fabF	β keto-acyl carrier protein synthase	Cerulenin	GCTGGATCCAATAGGAGGATAACGAATGAG (SEQ ID NO.: 78609); CAGGTCGACAATTATGCTTCAAATTTCTT (SEQ ID NO.: 78610)

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defB	Peptide deformylase	Actinonin	GCTGGATCCATAAGGAAGGTGCAATATATG (SEQ ID NO.: 78611); CAGGTCGACGTTTTAAACTTCTACTGCAT (SEQ ID NO.: 78612)
PBP-2a	Penicillin binding protein 2	Cloxacillin	GCCGGATCCCAAATGTAGTCTTATATAAGGAGGATATTGATG (SEQ ID NO.: 78613); CAGGTCGACGCTTCACTGTTTTGTTATTCATCTATATC (SEQ ID NO.: 78614)

* antibiotics unavailable commercially

1575

EXAMPLE 22

Overexpression of Genes Encoding Gene Products Required for Proliferation Confers Specific Resistance to Antibiotics which Target the Overexpressed Gene Product

To demonstrate that cells which overexpress a gene encoding a gene product required for proliferation are specifically resistant to antibiotics which target that gene product, the following experiments were performed. Several identical compound plates were prepared as described above in which different antibiotics were present in different wells. Media containing cells overexpressing different genes were separately dispensed into each one of these plates. Plate incubation and growth measurement were the same as described in Example 21 above. Growth was deemed specific if cells overexpressing one particular gene only gained resistance to antibiotics which target the product of the overexpressed gene but not to other antibiotics which target the products of genes which were not overexpressed.

As indicated in Figure 14 overexpression of the *fabI* gene conferred resistance to triclosan, which acts on the gene product of the *fabI* gene, enoyl-acyl carrier protein reductase. However, overexpression of the *fabI* gene did not confer resistance to cerulenin, trimethoprim, or actinonin, each of which act on other gene products.

Similarly, as indicated in Figure 15 overexpression of the *folA* gene conferred resistance to trimethoprim, which acts on the gene product of the *folA* gene, dihydrofolate reductase. However, overexpression of the *folA* gene did not confer resistance to triclosan, cerulenin, or actinonin, each of which act on other gene products.

As indicated in Figure 16 overexpression of the *defB* gene conferred resistance to actinonin, which acts on the gene product of the *defB* gene, peptide deformylase. However, overexpression of the *defB* gene did not confer resistance to cerulenin, trimethoprim, or triclosan, each of which act on other gene products.

As indicated in Figure 17 overexpression of the *fabF* gene conferred resistance to cerulenin, which acts on the gene product of the *fabF* gene, β keto-acyl carrier protein synthase II. However, overexpression of the *fabF* gene did not confer resistance to triclosan, trimethoprim, or actinonin, each of which act on other gene products.

Thus, overexpression of a gene encoding a gene product required for proliferation confers specific resistance to antibiotics which target the overexpressed gene product.

EXAMPLE 23

Selection of a Strain Overexpressing a Gene Encoding a Target Gene Product from a Mixture of Strains Overexpressing Genes Required for Proliferation

To confirm that a strain expressing the gene product targeted by an antibiotic can be selected from a mixture of strains which each overexpress a different gene required for

proliferation, the following experiment was performed. *S. aureus* strains overexpressing one of nine genes encoding a gene product required for proliferation were constructed as described above. The nine overexpressed genes were *fabF, defB, folA, fabI, ileS, fusA, gyrB, murA, rpoB*. A mixture of the nine strains was grown wells in a 96 well plate in medium containing various concentrations of inducer and a sufficient concentration of actinonin, cerulenin, triclosan or trimethoprim to inhibit the growth of strains which do not overexpress the targets of these antibiotics.

Growth was observed in wells containing appropriate inducer concentrations and each one of the four antibiotics (See Figure 18). The cultures which grew in the presence of one of the antibiotics were analyzed as follows. The cultures were removed from the wells of the plate and single colonies were obtained by plating serial dilutions LB agar plates containing an appropriate antibiotic. Plasmids were isolated from at least 60 individual colonies for each culture and the genes which conferred antibiotic resistance were amplified by performing PCR reactions using vector-specific primers. The PCR products were then sequenced.

All of the plasmids obtained from the culture which grew in the presence of cerulenin contained the *fabF* sequence. Similarly, all of the plasmids obtained from clones which grew in the presence of triclosan contained the *fabI* gene. All of the plasmid obtained from colonies which grew in the presence of actinonin contained the *defB* gene. In addition, 81% of the plasmids obtained from colonies which grew in the presence of trimethoprim contained the *folA* gene. Growth conditions could be further optimized to provide 100% recovery of plasmids containing the *folA* gene.

These results demonstrate that a strain expressing the gene product targeted by an antibiotic can be selected from a mixture of strains which each overexpress a different gene required for proliferation.

EXAMPLE 24

Identification of Amplification Products Having Distinguishable Lengths

The following genes were identified as being required for proliferation as previously described in U.S. Patent Application Serial Number 09/815,242, filed march 21, 2001. Plasmids in which antisense nucleic acids complementary to nucleotide sequences the essential *pbpC, secA, ylaO(Bs), yphC(Bs),trpS, polC, fabI, rpsR (Bs), fabF(yjaY), ileS, murC, fmhB, murA (Bs), murF(Bs), ftsZ, tufA, gyrA, rpoB, grlA or folA(dfrA)* genes were transcribed from the XylT5 promoter in *Staphylococcus aureus*.

Amplification primers were designed which would yield amplification products of the following lengths if the plasmid encoding the corresponding antisense nucleic acid is present in a mixture of nucleic acids:

yphC	260bp	*secA*	267bp
folA	230 bp	*tufA*	243bp
fabI	220bp	*gyrA*	225bp
trpS	208bp	*ileS*	215bp
fabF	189bp	*murF*	203bp
murA	176bp	*fmhB*	181bp
rpoB	159bp	*ylaO*	169bp
grlA	151bp	*pbpC*	156bp
murC	129bp	*polC*	145bp
rpsR	109bp	*ftsZ*	117bp

The 5' primer of each pair was complementary to a nucleotide sequence within the xylT5 promoter while 3' primer was complementary to a nucleotide sequence within the antisense clone. The 5' primer of each pair was identical for each amplification reaction. The nucleotide sequence GTTTCTT was appended on the 5' end of the 3' primers. One primer in each pair was labeled with either VIC or 6FAM.

Two sets of ten plasmids containing the antisense nucleic acids complementary to the genes listed in each of the columns above were mixed in equal amounts in 11 tubes except that either the plasmid encoding antisense nucleic acids complementary to a nucleotide sequence in the *grlA* gene or the plasmid encoding antisense nucleic acids complementary to nucleotide sequences in the *fmhB* gene were serially diluted two fold in each of the 11 tubes (i.e. the first tube had 100pg of the *grlA* plasmid or the fmhB plasmid while the last tube had 0.10pg of the *grlA* plasmid or the fmhB plasmid). Amplification reactions were conducted on the mixtures and the amplification products were separated on a 5% NuSieve 3:1 agarose gel (BioWhittaker Molecular Applications Rockland, ME). The levels of the 151bp or 181 amplification products for the grlA or fmhB primer respectively were specifically reduced in a stepwise fashion with increasing dilutions while the levels of the undiluted products remained constant. The assay readily detected a 10-fold decrease in template concentration reflected in the amplification products corresponding to the *grlA* or *fmhB* plasmids.

Although this method has been described using examples of antisense nucleic acids to specific essential genes, it will be appreciated that this method can be used with any of the antisense nucleic acids described herein, such as an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, an antisense nucleic acid comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a nucleic acid complementary to a nucleic acid comprising a nucleotide sequence

selected from the group consisting of SEQ ID NOs.: 6214-42397, a nucleic acid complementary to a nucleic acid comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397, a nucleic acid complementary to a nucleic acid which encodes a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42398-78581, a nucleic acid complementary to a nucleic acid which encodes at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids of a polypeptide sequence selected from the group consisting of SEQ ID NOs.: 42398-78581, a homologous antisense nucleic acid, an antisense nucleic acid comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of a homologous nucleic acid, a nucleic acid complementary to a homologous coding nucleic acid, a nucleic acid complementary to at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of a homologous coding nucleic acid, a nucleic acid complementary to a nucleic acid which encodes a homologous polypeptide, or a nucleic acid complementary to a nucleic acid which encodes at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids of a homologous polypeptide. It will also be appreciated that promoters other than XlyT5 can be used to express the gene products described herein. For example, a number of promoters useful for nucleic acid expression (including antisense nucleic acid expression) in *Enterococcus faecalis, Staphylococcus areus* as well as other Gram positive organisms are described in U.S. Patent Application Serial Number 10/032,393, filed December 21, 2001.

Additionally, the above methods can be used with any organism including *Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus*

mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis or any species falling within the genera of any of the above species.

EXAMPLE 25

Selective Disappearance of Amplification Products Corresponding to Strains Underexpressing a Gene Product on which a Compound which Inhibits Proliferation Acts

Strains of *Staphylococcus aureus* containing plasmids encoding antisense nucleic acids complementary to nucleotide sequences within the *yphC, folA, fabI, trpS, fabF, murA, rpoB, grlA, murC* or *rpsR* genes (described in Example 24 above) were mixed together in identical cultures such that the number of cells of each strain in the culture was identical. Each of the cultures containing the ten strains was contacted with one of the following antibiotics at one of the following concentrations:

spectinomycin- 2.5, 5.0ug/ml

mupriocin- 4.3, 8.6, 17.2ug/ml.

cerulenin- 4.5, 9.0, 18.0ug/ml

Spectinomycin acts on the product of the *rpsR* gene, mupriocin acts on the product of the *ileS* gene and cerulenin acts on the product of the *FabF* gene. The middle concentration for each antibiotic is its IC50.

The culture containing the ten strains were grown in rich medium (L-Broth; for antisense LB + chloroamphenicol to maintain antisense plasmid) until the cells reached early log phase then contacted with of one of the above-stated compounds at one of the concentrations listed above (preferably near IC50). The cultures were grown for a sufficient length of time to permit the compounds to specifically inhibit the growth of strains underexpressing their targets. Preferably the cultures were grown at least 16 hr, more preferably between 24 and 48 hrs. It is desirable to avoid allowing the culture to grow for time periods which might places selective pressure on the strains which could lead to false positives.

The cells were harvested by centrifugation and plasmid DNA was isolated from the cultures. PCR amplifications were performed as described in Example 24. Amplification products were run on NuSieve agarose gels as described above. The amounts of the amplification products corresponding to each antisense nucleic acid were determined and

compared to those in a control culture which was not contacted with the drug or to the amounts of the amplification products corresponding to the other antisense nucleic acids which were not complementary to nucleotide sequences in the genes encoding the gene products on which the compounds act. In each case, only the amplification product corresponding to the target on which the antibiotic acts was not detectable on the gel.

It is desirable, in embodiments in which the level or activity of gene products is regulated by transcribing antisense nucleic acids complementary to gene products required for proliferation or by replacing the native promoters of such genes with regulatable promoters, to perform dose-response curve for the inducer used to induce transcription of the antisense nucleic acids or induce transcription from the regulatable promoter. In such embodiments, it is desirable to use the lowest concentration of inducer which provides optimal transcription levels for detecting the effects of a particular test compound while interfering as little as possible with the growth of strains which do not overexpress or underexpress the target on which the compound acts. It also desirable contact the cultures with varying amounts of test compounds to determine the optimal amounts for obtaining differential growth of strains which overexpress or underexpress the targets on which the compounds act. Preferably, if the strains overexpress gene products required for proliferation, the level of the compound is preferably about IC_{90} or above . Preferably, if the strains underexpress gene products required for proliferation, the level of the compound is preferably about IC_{50} or below .

It will be appreciated that, if desired, the amplification products may be detected using the dyes described above. It will also be appreciated that amplification products may be detected using any desired amplification method including RT-PCR and PCR.

Although this method has been described using examples of antisense nucleic acids to specific essential genes, it will be appreciated that this method can be used with any of the antisense nucleic acids described herein, such as an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a nucleic acid sequence complementary to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397, a nucleic acid sequence complementary to a nucleic acid sequence which encodes a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42398-78581, a homologous antisense nucleic acid, a nucleic acid sequence complementary to a homologous coding nucleic acid, or a nucleic acid complementary to a nucleic acid which encodes a homologous polypeptide. It will also be appreciated that promoters other than XlyT5 can be used to express the gene products described herein. For example, a number of promoters useful for nucleic acid expression (including antisense nucleic acid expression) in *Enterococcus faecalis, Staphylococcus areus* as well as

other Gram positive organisms are described in U.S. Patent Application Serial Number 10/032,393, filed December 21, 2001.

Additionally, the above methods can be used with any organism including *Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis* or any species falling within the genera of any of the above species.

EXAMPLE 26

Use of Identified Nucleic Acid Sequences as Probes

The sequences from *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis,*

Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae or *Yersinia pestis* described herein, homologous coding nucleic acids, or homologous antisense nucleic acids can be used as probes to obtain the sequence of additional genes of interest from a second cell or microorganism. For example, probes to genes encoding potential bacterial target proteins may be hybridized to nucleic acids from other organisms including other bacteria and higher organisms, to identify homologous sequences in these other organisms. For example, the identified sequences from *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae* or *Yersinia pestis,* homologous coding nucleic acids, or homologous antisense nucleic acids may be used to identify homologous sequences in *Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum,*

Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis or any species falling within the genera of any of the above species. In some embodiments of the present invention, the nucleic acids from *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae* or *Yersinia pestis* described herein, homologous coding nucleic acids, or homologous antisense nucleic acids may be used to identify homologous nucleic acids from a heterologous organism other than *E. coli*.

Hybridization between the nucleic acids from *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae,*

Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae or *Yersinia pestis* described herein, homologous coding nucleic acids, or homologous antisense nucleic acids and nucleic acids from humans might indicate that the protein encoded by the gene to which the probe corresponds is found in humans and therefore not necessarily an optimal drug target. Alternatively, the gene can be conserved only in bacteria and therefore would be a good drug target for a broad spectrum antibiotic or antimicrobial. These probes can also be used in a known manner to isolate homologous nucleic acids from *Staphylococcus, Salmonella, Klebsiella, Pseudomonas, Enterococcus* or other cells or microorganisms, e.g. by screening a genomic or cDNA library.

Probes derived from the nucleic acid sequences from *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae* or *Yersinia pestis* described herein, homologous coding nucleic acids, or homologous antisense nucleic acids, or portions thereof, can be labeled with detectable labels familiar to those skilled in the art, including radioisotopes and non-radioactive labels, to provide a detectable probe. The detectable probe can be single stranded or double stranded and can be made using techniques known in the art, including *in vitro* transcription, nick translation, or kinase reactions. A nucleic acid sample containing a sequence capable of hybridizing to the labeled probe is contacted with the labeled probe. If the

nucleic acid in the sample is double stranded, it can be denatured prior to contacting the probe. In some applications, the nucleic acid sample can be immobilized on a surface such as a nitrocellulose or nylon membrane. The nucleic acid sample can comprise nucleic acids obtained from a variety of sources, including genomic DNA, cDNA libraries, RNA, or tissue samples.

Procedures used to detect the presence of nucleic acids capable of hybridizing to the detectable probe include well known techniques such as Southern blotting, Northern blotting, dot blotting, colony hybridization, and plaque hybridization. In some applications, the nucleic acid capable of hybridizing to the labeled probe can be cloned into vectors such as expression vectors, sequencing vectors, or in vitro transcription vectors to facilitate the characterization and expression of the hybridizing nucleic acids in the sample. For example, such techniques can be used to isolate, purify and clone sequences from a genomic library, made from a variety of bacterial species, which are capable of hybridizing to probes made from the sequences identified as decribed herein.

EXAMPLE 27

Preparation of PCR Primers and Amplification of DNA

The identified *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae* or *Yersinia pestis* genes corresponding directly to or located within the operon of nucleic acid sequences required for proliferation, homologous coding nucleic acids, or homologous antisense nucleic acids or portions thereof can be used to prepare PCR primers for a variety of applications, including the identification or isolation of homologous sequences from other species. For example, the *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni,*

Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae or *Yersinia pestis* genes may be used to prepare PCR primers to identify or isolate homologous sequences from *Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis* or any species falling within the genera of any of the above species. In some embodiments of the present invention, the PCR primers may be used to identify or isolate homologous nucleic acids from an organism other than *E. coli*.

The identified or isolated nucleic acids obtained using the PCR primers may contain part or all of the homologous nucleic acids. Because homologous nucleic acids are related but not identical in sequence, those skilled in the art will often employ degenerate sequence PCR primers. Such degenerate sequence primers are designed based on sequence regions that are either known to be conserved or suspected to be conserved such as conserved coding regions. The successful production of a PCR product using degenerate probes generated from the sequences identified herein would indicate the presence of a homologous gene sequence in the species being screened. The PCR primers are at least 10 nucleotides, and preferably at least 20 nucleotides in length. More preferably, the PCR primers are at least 20-30 nucleotides in length. In some embodiments, the PCR primers can be more than 30 nucleotides in length. It is preferred that the primer pairs have approximately the same G/C ratio, so that melting temperatures are approximately the same. A variety of PCR techniques are familiar to those skilled in the art. For a review of PCR technology, see Molecular Cloning to Genetic Engineering White, B.A. Ed. in **Methods in Molecular Biology** 67: Humana Press, Totowa 1997. When the entire coding sequence of the target gene is known, the 5' and 3' regions of the target gene can be used as the sequence source for PCR probe generation. In each of these PCR procedures, PCR primers on either side of the nucleic acid sequences to be amplified are added to a suitably prepared nucleic acid sample along with dNTPs and a thermostable polymerase such as Taq polymerase, Pfu polymerase, or Vent polymerase. The nucleic acid in the sample is denatured and the PCR primers are specifically hybridized to complementary nucleic acid sequences in the sample. The hybridized primers are extended. Thereafter, another cycle of denaturation, hybridization, and extension is initiated. The cycles are repeated multiple times to produce an amplified fragment containing the nucleic acid sequence between the primer sites.

EXAMPLE 28

Inverse PCR

The technique of inverse polymerase chain reaction can be used to extend the known nucleic acid sequence identified as described herein. The inverse PCR reaction is described generally by Ochman et al., in Ch. 10 of **PCR Technology: Principles and Applications for DNA Amplification**, (Henry A. Erlich, Ed.) W.H. Freeman and Co. (1992). Traditional PCR requires two primers that are used to prime the synthesis of complementary strands of DNA. In inverse PCR, only a core sequence need be known.

Using the sequences identified as relevant from the techniques taught in Examples 10 and 11 and applied to other species of bacteria, a subset of nucleic sequences are identified that correspond to genes or operons that are required for bacterial proliferation. In species for which a genome sequence is not known, the technique of inverse PCR provides a method for obtaining the

gene in order to determine the sequence or to place the probe sequences in full context to the target sequence to which the identified nucleic acid sequence binds.

To practice this technique, the genome of the target organism is digested with an appropriate restriction enzyme so as to create fragments of nucleic acid that contain the identified sequence as well as unknown sequences that flank the identified sequence. These fragments are then circularized and become the template for the PCR reaction. PCR primers are designed in accordance with the teachings of Example 27 and directed to the ends of the identified sequence.. The primers direct nucleic acid synthesis away from the known sequence and toward the unknown sequence contained within the circularized template. After the PCR reaction is complete, the resulting PCR products can be sequenced so as to extend the sequence of the identified gene past the core sequence of the identified exogenous nucleic acid sequence identified. In this manner, the full sequence of each novel gene can be identified. Additionally the sequences of adjacent coding and noncoding regions can be identified.

EXAMPLE 29

Identification of Genes Required for *Escherichia coli* Proliferation

Genes required for proliferation in *Escherichia coli* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 30

Identification of Genes Required for *Staphylococcus aureus* Proliferation

Genes required for proliferation in *Staphylococcus aureus* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 31

Identification of Genes Required for *Enterococcus faecalis* Proliferation

Genes required for proliferation in *Enterococcus faecalis* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 32

Identification of Genes Required for *Klebsiella pneumoniae* Proliferation

Genes required for proliferation in *Klebsiella pneumoniae* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 33

Identification of Genes Required for *Pseudomonas aeruginosa* Proliferation

Genes required for proliferation in *Pseudomonas aeruginosa* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 34

Identification of Genes Required for *Salmonella typhimurium* Proliferation

Genes required for proliferation in *Salmonella typhimurium* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 35

Identification of Genes Required for *Acinetobacter baumannii* Proliferation

Genes required for proliferation in *Acinetobacter baumannii* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 36

Identification of Genes Required for *Bacillus anthracis* Proliferation

Genes required for proliferation in *Bacillus anthracis* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 37

Identification of Genes Required for *Bordetella pertussis* Proliferation

Genes required for proliferation in *Bordetella pertussis* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 38

Identification of Genes Required for *Borrelia burgdorferi* Proliferation

Genes required for proliferation in *Borrelia burgdorferi* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 39

Identification of Genes Required for *Burkholderia cepacia* Proliferation

Genes required for proliferation in *Burkholderia cepacia* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 40

Identification of Genes Required for *Burkholderia fungorum* Proliferation

Genes required for proliferation in *Burkholderia fungorum* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 41

Identification of Genes Required for *Burkholderia mallei* Proliferation

Genes required for proliferation in *Burkholderia mallei* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 42

Identification of Genes Required for *Campylobacter jejuni* Proliferation

Genes required for proliferation in *Campylobacter jejuni* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 43

Identification of Genes Required for *Chlamydia pneumoniae* Proliferation

Genes required for proliferation in *Chlamydia pneumoniae* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 44

Identification of Genes Required for *Chlamydia trachomatis* Proliferation

Genes required for proliferation in *Chlamydia trachomatis* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 45

Identification of Genes Required for *Clostridium acetobutylicum* Proliferation

Genes required for proliferation in *Clostridium acetobutylicum* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 46

Identification of Genes Required for *Clostridium botulinum* Proliferation

Genes required for proliferation in *Clostridium botulinum* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 47

Identification of Genes Required for *Clostridium difficile* Proliferation

Genes required for proliferation in *Clostridium difficile* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 48

Identification of Genes Required for *Corynebacterium diptheriae* Proliferation

Genes required for proliferation in *Corynebacterium diptheriae* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 49

Identification of Genes Required for *Enterobacter cloacae* Proliferation

Genes required for proliferation in *Enterobacter cloacae* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 50

Identification of Genes Required for *Enterococcus faecium* Proliferation

Genes required for proliferation in *Enterococcus faecium* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 51

Identification of Genes Required for *Haemophilus influenzae* Proliferation

Genes required for proliferation in *Haemophilus influenzae* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 52

Identification of Genes Required for *Helicobacter pylori* Proliferation

Genes required for proliferation in *Helicobacter pylori* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 53

Identification of Genes Required for *Legionella pneumophila* Proliferation

Genes required for proliferation in *Legionella pneumophila* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 54

Identification of Genes Required for *Listeria monocytogenes* Proliferation

Genes required for proliferation in *Listeria monocytogenes* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 55

Identification of Genes Required for *Moraxella catarrhalis* Proliferation

Genes required for proliferation in *Moraxella catarrhalis* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 56

Identification of Genes Required for *Mycobacterium avium* Proliferation

Genes required for proliferation in *Mycobacterium avium* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 57

Identification of Genes Required for *Mycobacterium bovis* Proliferation

Genes required for proliferation in *Mycobacterium bovis* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 58

Identification of Genes Required for *Mycobacterium leprae* Proliferation

Genes required for proliferation in *Mycobacterium leprae* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 59

Identification of Genes Required for *Mycobacterium tuberculosis* Proliferation

Genes required for proliferation in *Mycobacterium tuberculosis* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 60

Identification of Genes Required for *Mycoplasma genitalium* Proliferation

Genes required for proliferation in *Mycoplasma genitalium* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 61

Identification of Genes Required for *Mycoplasma pneumoniae* Proliferation

Genes required for proliferation in *Mycoplasma pneumoniae* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 62

Identification of Genes Required for *Neisseria gonorrhoeae* Proliferation

Genes required for proliferation in *Neisseria gonorrhoeae* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 63

Identification of Genes Required for *Neisseria meningitidis* Proliferation

Genes required for proliferation in *Neisseria meningitidis* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 64

Identification of Genes Required for *Pasteurella multocida* Proliferation

Genes required for proliferation in *Pasteurella multocida* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 65

Identification of Genes Required for *Proteus mirabilis* Proliferation

Genes required for proliferation in *Proteus mirabilis* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 66

Identification of Genes Required for *Pseudomonas putida* Proliferation

Genes required for proliferation in *Pseudomonas putida* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 67

Identification of Genes Required for *Pseudomonas syringae* Proliferation

Genes required for proliferation in *Pseudomonas syringae* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 68

Identification of Genes Required for *Salmonella paratyphi* Proliferation

Genes required for proliferation in *Salmonella paratyphi* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 69

Identification of Genes Required for *Salmonella typhi* Proliferation

Genes required for proliferation in *Salmonella typhi* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 70

Identification of Genes Required for *Staphylococcus epidermidis* Proliferation

Genes required for proliferation in *Staphylococcus epidermidis* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 71

Identification of Genes Required for *Staphylococcus haemolyticus* Proliferation

Genes required for proliferation in *Staphylococcus haemolyticus* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 72

Identification of Genes Required for *Streptococcus mutans* Proliferation

Genes required for proliferation in *Streptococcus mutans* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 73

Identification of Genes Required for *Streptococcus pneumoniae* Proliferation

Genes required for proliferation in *Streptococcus pneumoniae* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 74

Identification of Genes Required for *Streptococcus pyogenes* Proliferation

Genes required for proliferation in *Streptococcus pyogenes* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 75

Identification of Genes Required for *Treponema pallidum* Proliferation

Genes required for proliferation in *Treponema pallidum* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 76

Identification of Genes Required for *Ureaplasma urealyticum* Proliferation

Genes required for proliferation in *Ureaplasma urealyticum* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 77

Identification of Genes Required for *Vibrio cholerae* Proliferation

Genes required for proliferation in *Vibrio cholerae* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 78

Identification of Genes Required for *Yersinia pestis* Proliferation

Genes required for proliferation in *Yersinia pestis* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 79

Identification of Genes Required for *Salmonella enterica* Proliferation

Genes required for proliferation in *Salmonella enterica* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 80

Identification of Genes Required for *Aspergillus fumigatus* Proliferation

Genes required for proliferation in *Aspergillus fumigatus* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 81

Identification of Genes Required for *Plasmodium ovale* Proliferation

Genes required for proliferation in *Plasmodium ovale* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 82

Identification of Genes Required for *Entamoeba histolytica* Proliferation

Genes required for proliferation in *Entamoeba histolytica* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 83

Identification of Genes Required for *Candida albicans* Proliferation

Genes required for proliferation in *Candida albicans* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 84

Identification of Genes Required for *Histoplasma capsulatum* Proliferation

Genes required for proliferation in *Histoplasma capsulatum* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

EXAMPLE 85

Identification of Genes Required for *Salmonella cholerasuis* Proliferation

Genes required for proliferation in *Salmonella cholerasuis* are identified according to the methods described above. For example, promoters and vectors described herein can be used to identify essential genes described herein.

Use of Isolated Exogenous Nucleic Acid Fragments as Antisense Antibiotics

In addition to using the identified sequences to enable screening of molecule libraries to identify compounds useful to identify antibiotics, antisense nucleic acids complementary to the proliferation-required sequences or portions thereof, antisense nucleic acids complementary to homologous coding nucleic acids, or homologous antisense nucleic acids can be used as therapeutic agents. Specifically, the proliferation-required sequences or homolgous coding nucleic acids, or portions therof, in an antisense orientation or homologous antisense nucleic acids can be provided to an individual to inhibit the translation of a bacterial target gene or the processing, folding, or assembly into a protein/RNA complex of a nontranslated RNA.

EXAMPLE 86

Generation of Antisense Therapeutics from Identified Exogenous Sequences

Antisense nucleic acids complementary to the proliferation-required sequences described herein, or portions thereof, antisense nucleic acids complementary to homologous coding nucleic acids, or portions thereof, or homologous antisense nucleic acids or portions thereof can be used as antisense therapeutics for the treatment of bacterial infections or simply

for inhibition of bacterial growth *in vitro* or *in vivo*. For example, the antisense therapeutics may be used to treat bacterial infections caused by *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae* or *Yersinia pestis* or to inhibit the growth of these organisms. The antisense therapeutics may also be used to treat infections caused by or to inhibit the growth of *Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus,*

Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis or any species falling within the genera of any of the above species. In some embodiments of the present invention, the antisense therapuetics may be used to treat infection by or inhibit the growth of an organism other than *E. coli*.

The therapy exploits the biological process in cells where genes are transcribed into messenger RNA (mRNA) that is then translated into proteins. Antisense RNA technology contemplates the use of antisense nucleic acids, including antisense oligonucleotides, complementary to a target gene that will bind to its target nucleic acid and decrease or inhibit the expression of the target gene. For example, the antisense nucleic acid may inhibit the translation or transcription of the target nucleic acid. In one embodiment, antisense oligonucleotides can be used to treat and control a bacterial infection of a cell culture containing a population of desired cells contaminated with bacteria. In another embodiment, the antisense oligonucleotides can be used to treat an organism with a bacterial infection.

Antisense oligonucleotides can be synthesized from any of the sequences of the present invention using methods well known in the art. In a preferred embodiment, antisense oligonucleotides are synthesized using artificial means. Uhlmann & Peymann, Chemical Rev. 90:543-584 (1990) review antisense oligonucleotide technology in detail. Modified or unmodified antisense oligonucleotides can be used as therapeutic agents. Modified antisense oligonucleotides are preferred. Modification of the phosphate backbones of the antisense oligonucleotides can be achieved by substituting the internucleotide phosphate residues with methylphosphonates, phosphorothioates, phosphoramidates, and phosphate esters. Nonphosphate internucleotide analogs such as siloxane bridges, carbonate brides, thioester bridges, as well as many others known in the art may also be used. The preparation of certain antisense oligonucleotides with modified internucleotide linkages is described in U.S. Patent No. 5,142,047.

Modifications to the nucleoside units of the antisense oligonucleotides are also contemplated. These modifications can increase the half-life and increase cellular rates of uptake for the oligonucleotides *in vivo*. For example, α-anomeric nucleotide units and modified nucleotides such as 1,2-dideoxy-d-ribofuranose, 1,2-dideoxy-1-phenylribofuranose, and N^4, N^4-ethano-5-methyl-cytosine are contemplated for use in the present invention.

An additional form of modified antisense molecules is found in peptide nucleic acids. Peptide nucleic acids (PNA) have been developed to hybridize to single and double stranded nucleic acids. PNA are nucleic acid analogs in which the entire deoxyribose-phosphate backbone

has been exchanged with a chemically different, but structurally homologous, polyamide (peptide) backbone containing 2-aminoethyl glycine units. Unlike DNA, which is highly negatively charged, the PNA backbone is neutral. Therefore, there is much less repulsive energy between complementary strands in a PNA-DNA hybrid than in the comparable DNA-DNA hybrid, and consequently they are much more stable. PNA can hybridize to DNA in either a Watson/Crick or Hoogsteen fashion (Demidov et al., *Proc. Natl. Acad. Sci. U.S.A.* **92**:2637-2641, 1995; Egholm, *Nature* **365**:566-568, 1993; Nielsen et al., *Science* **254**:1497-1500, 1991; Dueholm et al., *New J. Chem.* **21**:19-31, 1997).

Molecules called PNA "clamps" have been synthesized which have two identical PNA sequences joined by a flexible hairpin linker containing three 8-amino-3,6-dioxaoctanoic acid units. When a PNA clamp is mixed with a complementary homopurine or homopyrimidine DNA target sequence, a PNA-DNA-PNA triplex hybrid can form which has been shown to be extremely stable (Bentin et al., *Biochemistry* **35**:8863-8869, 1996; Egholm et al., *Nucleic Acids Res.* **23**:217-222, 1995; Griffith et al., *J. Am. Chem. Soc.* **117**:831-832, 1995).

The sequence-specific and high affinity duplex and triplex binding of PNA have been extensively described (Nielsen et al., *Science* **254**:1497-1500, 1991; Egholm et al., *J. Am. Chem. Soc.* **114**:9677-9678, 1992; Egholm et al., *Nature* **365**:566-568, 1993; Almarsson et al., *Proc. Natl. Acad. Sci. U.S.A.* **90**:9542-9546, 1993; Demidov et al., *Proc. Natl. Acad. Sci. U.S.A.* **92**:2637-2641, 1995). They have also been shown to be resistant to nuclease and protease digestion (Demidov et al., *Biochem. Pharm.* **48**:1010-1313, 1994). PNA has been used to inhibit gene expression (Hanvey et al., *Science* **258**:1481-1485,1992; Nielsen et al., *Nucl. Acids. Res.*, **21**:197-200, 1993; Nielsen et al., *Gene* **149**:139-145, 1994; Good & Nielsen, **Science**, 95: 2073-2076, 1998; to block restriction enzyme activity (Nielsen et al., *supra.*, 1993), to act as an artificial transcription promoter (Mollegaard, *Proc. Natl. Acad. Sci. U.S.A.* **91**:3892-3895, 1994) and as a pseudo restriction endonuclease (Demidov et al., *Nucl. Acids. Res.* **21**:2103-2107, 1993). Recently, PNA has also been shown to have antiviral and antitumoral activity mediated through an antisense mechanism (Norton, *Nature Biotechnol.*, **14**:615-619, 1996; Hirschman et al., *J. Investig. Med.* **44**:347-351, 1996). PNAs have been linked to various peptides in order to promote PNA entry into cells (Basu et al., *Bioconj. Chem.* **8**:481-488, 1997; Pardridge et al., *Proc. Natl. Acad. Sci. U.S.A.* **92**:5592-5596, 1995).

The antisense oligonucleotides contemplated by the present invention can be administered by direct application of oligonucleotides to a target using standard techniques well known in the art. The antisense oligonucleotides can be generated within the target using a plasmid, or a phage. Alternatively, the antisense nucleic acid may be expressed from a sequence in the chromosome of the target cell. For example, a promoter may be introduced into

the chromosome of the target cell near the target gene such that the promoter directs the transcription of the antisense nucleic acid. Alternatively, a nucleic acid containing the antisense sequence operably linked to a promoter may be introduced into the chromosome of the target cell. It is further contemplated that the antisense oligonucleotides are incorporated in a ribozyme sequence to enable the antisense to specifically bind and cleave its target mRNA. For technical applications of ribozyme and antisense oligonucleotides see Rossi et al., **Pharmacol. Ther. 50(2)**:245-254, (1991). The present invention also contemplates using a retron to introduce an antisense oligonucleotide to a cell. Retron technology is exemplified by U.S. Patent No. 5,405,775. Antisense oligonucleotides can also be delivered using liposomes or by electroporation techniques which are well known in the art.

The antisense nucleic acids described above can also be used to design antibiotic compounds comprising nucleic acids which function by intracellular triple helix formation. Triple helix oligonucleotides are used to inhibit transcription from a genome. The antisense nucleic acids can be used to inhibit cell or microorganism gene expression in individuals infected with such microorganisms or containing such cells. Traditionally, homopurine sequences were considered the most useful for triple helix strategies. However, homopyrimidine sequences can also inhibit gene expression. Such homopyrimidine oligonucleotides bind to the major groove at homopurine:homopyrimidine sequences. Thus, both types of sequences based on the sequences from *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae* or *Yersinia pestis* or homologous nucleic acids that are required for proliferation are contemplated for use as antibiotic compound templates.

The antisense nucleic acids, such as antisense oligonucleotides, which are complementary to the proliferation-required nucleic acids from *Escherichia coli,*

Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae or *Yersinia pestis* or to homologous coding nucleic acids, or portions thereof, may be used to induce bacterial cell death or at least bacterial stasis by inhibiting target nucleic acid transcription or translation. Antisense oligonucleotides complementary to about 8 to 40 nucleotides of the proliferation-required nucleic acids described herein or homologous coding nucleic acids have sufficient complementarity to form a duplex with the target sequence under physiological conditions.

To kill bacterial cells or inhibit their growth, the antisense oligonucleotides are applied to the bacteria or to the target cells under conditions that facilitate their uptake. These conditions include sufficient incubation times of cells and oligonucleotides so that the antisense oligonucleotides are taken up by the cells. In one embodiment, an incubation period of 7-10 days is sufficient to kill bacteria in a sample. An optimum concentration of antisense oligonucleotides is selected for use.

The concentration of antisense oligonucleotides to be used can vary depending on the type of bacteria sought to be controlled, the nature of the antisense oligonucleotide to be used, and the relative toxicity of the antisense oligonucleotide to the desired cells in the treated culture. Antisense oligonucleotides can be introduced to cell samples at a number of different concentrations preferably between $1x10^{-10}$M to $1x10^{-4}$M. Once the minimum concentration that can adequately control gene expression is identified, the optimized dose is translated into a dosage suitable for use *in vivo*. For example, an inhibiting concentration in culture of $1x10^{-7}$ translates into a dose of approximately 0.6 mg/kg body weight. Levels of oligonucleotide approaching 100 mg/kg body weight or higher may be possible after testing the toxicity of the oligonucleotide in laboratory animals. It is additionally contemplated that cells from the subject are removed, treated with the

antisense oligonucleotide, and reintroduced into the subject. This range is merely illustrative and one of skill in the art are able to determine the optimal concentration to be used in a given case.

After the bacterial cells have been killed or controlled in a desired culture, the desired cell population may be used for other purposes.

EXAMPLE 87

Use of Antisense Oligonucleotides to Treat Contaminated Cell Cultures

The following example demonstrates the ability of an *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae* or *Yersinia pestis* antisense oligonucleotide or an antisense oligonucleotide complementary to a homologous coding nucleic acid, or portions thereof, to act as a bacteriocidal or bacteriostatic agent to treat a contaminated cell culture system. The application of the antisense oligonucleotides of the present invention are thought to inhibit the translation of bacterial gene products required for proliferation. The antisense nucleic acids may also inhibit the transcription, folding or processing of the target RNA.

In one embodiment of the present invention, the antisense oligonucleotide may comprise a phosphorothioate modified nucleic acid comprising at least about 15, at least about 20, at least about 25, at least about 30, at least about 35, at least about 40, or more than 40 consecutive nucleotides of an antisense nucleic acid listed in Table IA (SEQ ID NOs.: 1-6213). A sense oligodeoxynucleotide complementary to the antisense sequence is synthesized and used as a control. The oligonucleotides are synthesized and purified according to the procedures of Matsukura, et al., Gene 72:343 (1988). The test oligonucleotides are dissolved in a small volume of autoclaved water and added to culture medium to make a 100 micromolar stock solution.

Human bone marrow cells are obtained from the peripheral blood of two patients and cultured according standard procedures well known in the art. The culture is contaminated with *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae* or *Yersinia pestis* or an organism containing a homologous nucleic acid and incubated at 37°C overnight to establish bacterial infection.

The control and antisense oligonucleotide containing solutions are added to the contaminated cultures and monitored for bacterial growth. After a 10 hour incubation of culture and oligonucleotides, samples from the control and experimental cultures are drawn and analyzed for the translation of the target bacterial gene using standard microbiological techniques well known in the art. The target *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae* or *Yersinia pestis* gene or an

organism containing the homologous coding nucleic acid is found to be translated in the control culture treated with the control oligonucleotide, however, translation of the target gene in the experimental culture treated with the antisense oligonucleotide of the present invention is not detected or reduced, indicating that the culture is no longer contaminated or is contaminated at a reduced level.

EXAMPLE 88

Use of Antisense Oligonucleotides to Treat Infections

A subject suffering from a *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Yersinia pestis* infection or an infection with an organism containing a homologous coding nucleic acid is treated with the antisense oligonucleotide preparation above. The antisense oligonucleotide is provided in a pharmaceutically acceptable carrier at a concentration effective to inhibit the transcription or translation of the target nucleic acid. The present subject is treated with a concentration of antisense oligonucleotide sufficient to achieve a blood concentration of about 0.1-100 micromolar. The patient receives daily injections of antisense oligonucleotide to maintain this concentration for a period of 1 week. At the end of the week a blood sample is drawn and analyzed for the presence or absence of the organism using standard techniques well known in the art. There is no detectable evidence of *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae,*

Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Yersinia pestis or an organim containing a homologous coding nucleic acid and the treatment is terminated.

Antisense nucleic acids complementary to a homologous coding nucleic acid or a portion thereof may be used in the preceding method to treat individuals infected with an organism containing the homologous coding nucleic acid.

EXAMPLE 89

Preparation and Use of Triple Helix Forming Oligonucleotides

The sequences of proliferation-required nucleic acids, homologous coding nucleic acids, or homologous antisense nucleic acids are scanned to identify 10-mer to 20-mer homopyrimidine or homopurine stretches that could be used in triple-helix based strategies for inhibiting gene expression. Following identification of candidate homopyrimidine or homopurine stretches, their efficiency in inhibiting gene expression is assessed by introducing varying amounts of oligonucleotides containing the candidate sequences into a population of bacterial cells that normally express the target gene. The oligonucleotides may be prepared on an oligonucleotide synthesizer or they may be purchased commercially from a company specializing in custom oligonucleotide synthesis.

The oligonucleotides can be introduced into the cells using a variety of methods known to those skilled in the art, including but not limited to calcium phosphate precipitation, DEAE-Dextran, electroporation, liposome-mediated transfection or native uptake.

Treated cells are monitored for a reduction in proliferation using techniques such as monitoring growth levels as compared to untreated cells using optical density measurements. The oligonucleotides that are effective in inhibiting gene expression in cultured cells can then be introduced *in vivo* using the techniques well known in that art at a dosage level shown to be effective.

In some embodiments, the natural (beta) anomers of the oligonucleotide units can be replaced with alpha anomers to render the oligonucleotide more resistant to nucleases. Further, an intercalating agent such as ethidium bromide, or the like, can be attached to the 3' end of the alpha oligonucleotide to stabilize the triple helix. For information on the generation of oligonucleotides

suitable for triple helix formation see Griffin et al. (**Science 245**:967-971 (1989), which is hereby incorporated by this reference).

EXAMPLE 90

Identification of Bacterial Strains from Isolated Specimens by PCR

Classical bacteriological methods for the detection of various bacterial species are time consuming and costly. These methods include growing the bacteria isolated from a subject in specialized medium, cultivation on selective agar medium, followed by a set of confirmation assays that can take from 8 to 10 days or longer to complete. Use of the identified sequences of the present invention provides a method to dramatically reduce the time necessary to detect and identify specific bacterial species present in a sample.

In one exemplary method, bacteria are grown in enriched medium and DNA samples are isolated from specimens of, for example, blood, urine, stool, saliva or central nervous system fluid by conventional methods. A panel of PCR primers based on identified sequences unique to various species or types of cells or microorganisms are then utilized in accordance with Example 27 to amplify DNA of approximately 100-200 nucleotides in length from the specimen. A separate PCR reaction is set up for each pair of PCR primers and after the PCR reaction is complete, the reaction mixtures are assayed for the presence of PCR product. The presence or absence of bacteria from the species to which the PCR primer pairs belong is determined by the presence or absence of a PCR product in the various test PCR reaction tubes.

Although the PCR reaction is used to assay the isolated sample for the presence of various bacterial species, other assays such as the Southern blot hybridization are also contemplated.

Compounds which inhibit the activity or reduce the amount of gene products required for proliferation may be identified using rational drug design. These methods may be used with the proliferation-required polypeptides described herein or homologous polypeptides. In such methods, the structure of the gene product is determined using methods such as x-ray crystallography, NMR, or computer modelling. Compounds are screened to identify those which have a structure which allows them to interact with the gene product. In some embodiments, the compounds are screened to identify those which have structures which allow them to interact with regions of the gene product which are important for its activity. For example, the compounds may be screened to identify those which have structures which allow them to bind to the active site of the gene product to inhibit its activity. For example, the compound may be a suicide substrate which binds to the active site with high affinity, thereby preventing the gene product from acting on its natural substrate. Alternatively, the compound may bind to a region of the gene product which is involved in complex formation with other biomolecules. In such instances, the activity of the

gene product is inhibited by blocking the interaction between the gene product and other members of the complex.

Thus, one embodiment of the present invention comprises a method of using a crystal of the gene products of the present invention and/or a dataset comprising the three-dimensional coordinates obtained from the crystal in a drug-screening assay. The present invention also includes agents (modulators or drugs) that are identified by the methods of the present invention, along with the method of using agents (modulators or drugs) identified by a method of the present invention, for inhibiting the activity of or modulating the amount of an essential gene product. The present invention also includes crystals comprising the gene products of the present invention or portions thereof.

In some embodiments of the present invention, the three-dimensional structure of the polypeptides required for proliferation is determined using X-ray crystallography or NMR. The coordinates of the determined structure are used in computer-assisted modeling programs to identify compounds that bind to and/or modulate the activity or amount of the encoded polypeptide. The method may include the following steps: 1) the generation of high-purity crystals of the encoded recombinant (or endogenous) polypeptide for analysis; 2) determination of the three-dimensional structure of the polypeptide; and, 3) the use of computer-assisted "docking" programs to analyze the molecular interaction of compound structure and the polypeptide (i.e., drug screening).

General methods for performing each of the above steps are described below and are also well known to those of skill in the art. Any method known to those of skill in the art, including those described herein, may be employed for generating the three-dimensional structure for each identified essential gene product and its use in the drug-screening assays.

Crystals of the gene products required for proliferation may be obtained as follows. Under certain conditions, molecules condense from solution into a highly-ordered crystalline lattice, which is defined by a unit cell, the smallest repeating volume of the crystalline array. The contents of such a cell can interact with and diffract certain electromagnetic and particle waves (e.g., X-rays, neutron beams, electron beams etc.). Due to the symmetry of the lattice, the diffracted waves interact to create a diffraction pattern. By measuring the diffraction pattern, crystallographers are able to reconstruct the three-dimensional structure of the atoms in the crystal.

Any method known to those of skill in the art, including those set forth below, may be employed to prepare high-purity crystals. For example, crystals of the product of the identified essential gene can be grown by a number of techniques including batch crystallization, vapor diffusion (either by sitting drop or hanging drop) and by microdialysis. Seeding of the crystals

in some instances is required to obtain X-ray quality crystals. Standard micro and/or macro seeding of crystals may therefore be used. Exemplified below is the hanging-drop vapor diffusion procedure. Hanging drops of an essential gene product (2.5 µl, 10 mg/ml) in 20 mM Tris, pH=8.0, 100 mM NaCl are mixed with an equal amount of reservoir buffer containing 2.7-3.2 M sodium formate and 100 mM Tris buffer, pH=8.0, and kept at 4°C. Crystal showers may appear after 1-2 days with large single crystals growing to full size (0.3 X 0.3 X 0.15 mm^3) within 2-3 weeks. Crystals are harvested in 3.5 M sodium formate and 100 mM Tris buffer, pH=8.0 and cryoprotected in 3.5 M sodium formate, 100 mM Tris buffer, pH=8.0, 10% (w/v) sucrose, and 10% (v/v) ethylene glycol before flash freezing in liquid propane. In some embodiments, the crystal may be obtained using the methods described in U.S. Patent No. 5,869,604. The method involves (a) contacting a mixture containing uncrystallized polypeptides with an exogenous nucleating agent that has an areal lattice match of at least 90.4% to the polypeptide,(b) crystallizing the polypeptides, thereby forming at least one crystal of the polypeptide attached to the nucleating agent, the attached crystal being of a high purity, and at least one polypeptide crystal unattached to the nucleating agent, the unattached crystal being of a lower purity than the attached crystal, and (c) separating the crystal attached to the nucleating agent from the crystal unattached to the nucleating agent. The crystallized polypeptide may also be purified from contaminants by (a) contacting a mixture containing uncrystallized polypeptides and a contaminant with an exogenous nucleating agent that has an areal lattice match of at least 90.4% to the polypeptide, (b) crystallizing the polypeptides, thereby forming at least one crystal of the polypeptide attached to the nucleating agent, the attached crystal being of a high purity and produced in a high yield, and at least one crystal unattached to the nucleating agent, the unattached crystal being of a lower purity than the attached crystal, and (c) separating the crystal attached to the nucleating agent from the crystal unattached to the nucleating agent.

Once a crystal of the present invention is grown, X-ray diffraction data can be collected using methods familiar to those skilled in the art. Therefore, any person with skill in the art of protein crystallization having the present teachings and without undue experimentation can crystallize a large number of alternative forms of the essential gene products from a variety of different organisms, or polypeptides having conservative substitutions in their amino acid sequence.

A crystal lattice is defined by the symmetry of its unit cell and any structural motifs the unit cell contains. For example, there are 230 possible symmetry groups for an arbitrary crystal lattice, while the unit cell of the crystal lattice group may have an arbitrary dimension that depends on the molecules making up the lattice. Biological macromolecules, however, have

asymmetric centers and are limited to 65 of the 230 symmetry groups. See Cantor et al., Biophysical Chemistry, Vol. III, W. H. Freeman & Company (1980).

A crystal lattice interacts with electromagnetic or particle waves, such as X-rays or electron beams respectively, that have a wavelength with the same order of magnitude as the spacing between atoms in the unit cell. The diffracted waves are measured as an array of spots on a detection surface positioned adjacent to the crystal. Each spot has a three-dimensional position, hkl, and an intensity, I(hkl), both of which are used to reconstruct the three-dimensional electron density of the crystal with the so-called Electron Density Equation. The Electron Density Equation states that the three-dimensional electron density of the unit cell is the Fourier transform of the structure factors. Thus, in theory, if the structure factors are known for a sufficient number of spots in the detection space, then the three-dimensional electron density of the unit cell could be calculated using the Electron Density Equation.

In some embodiments of the present invention, an image of a crystal of a gene product required for proliferation or a portion thereof is obtained with the aid of a digital computer and the crystal's diffraction pattern as described in U.S. Patent No. 5,353,236. The diffraction pattern contains a plurality of reflections, each having an associated resolution. The image is obtained by (a) converting the diffraction pattern of the crystal into computer usable normalized amplitudes, the pattern being produced with a diffractometer; (b) determining from the diffraction pattern a dimension of a unit cell of the crystal; (c) providing an envelope defining the region of the unit cell occupied by the gene product or portion thereof in the crystal; (d) distributing a collection of scattering bodies within said envelope, the collection of scattering bodies having various arrangements, each of which has an associated pattern of Fourier amplitudes; (e) condensing the collection of scattering bodies to a condensed arrangement that results in a high correlation between a diffraction pattern and the pattern of Fourier amplitudes for said collection of scattering bodies; (f) determining the phase associated with at least one of the reflections of said diffraction pattern from the condensed arrangement of scattering bodies; (g) calculating an electron density distribution of the gene product or portion thereof within the unit cell from the phase determined in procedure f; and (h) displaying a graphical image of the gene product or portion thereof constructed from said electron density distribution.

The crystals of the gene products required for proliferation may be used in drug screening methods such as those described in U.S. Patent Number 6,156,526. Briefly, in such methods, a compound which inhibits the formation of a complex comprising the gene product or a portion thereof is identified as follows. A set of atomic coordinates defining the three-dimensional structure of a complex including the gene product of interest or a portion thereof are determined. A potential compound that binds to the gene product or a portion thereof

involved in complex formation is selected using the atomic coordinates obtained above. The compound is contacted with the gene product or portion thereof and its binding partner(s) in the complex under conditions which would permit the complex to form in the absence of the potential compound. The binding affinity of the gene product or portion thereof for its binding partner(s) is determined and a potential compound is identified as a compound that inhibits the formation of the complex when there is a decrease in the binding affinity of the gene product or portion thereof for its binding partner(s).

In some embodiments of the present invention, the three dimensional structure of the essential gene product is determined and potential agonists and/or potential antagonists are designed with the aid of computer modeling [Bugg et al., Scientific American, Dec.:92-98 (1993); West et al., TIPS, 16:67-74 (1995); Dunbrack et al., Folding & Design, 2:27-42 (1997).

Computer analysis may be performed with one or more of the computer programs including: QUANTA, CHARMM, INSIGHT, SYBYL, MACROMODEL and ICM [Dunbrack et al., Folding & Design, 2:27-42 (1997)]. . In a further embodiment of this aspect of the invention, an initial drug-screening assay is performed using the three-dimensional structure so obtained, preferably along with a docking computer program. Such computer modeling can be performed with one or more Docking programs such as FlexX, DOC, GRAM and AUTO DOCK [Dunbrack et al., Folding & Design, 2:27-42 (1997)].

It should be understood that for each drug screening assay provided herein, a number of iterative cycles of any or all of the steps may be performed to optimize the selection. The drug screening assays of the present invention may use any of a number of means for determining the interaction between an agent or drug and an essential gene product.

In some embodiments of the present invention, a drug can be specifically designed to bind to an essential gene product of the present invention through NMR based methodology. [Shuker et al., pi Science 274:1531-1534 (1996)]. NMR spectra may be recorded using devices familiar to those skilled in the art, such as the Varian Unity Plus 500 and unity 600 spectrometers, each equipped with a pulsed-field gradient triple resonance probe as analyzed as described in Bagby et al., [Cell 82:857-867 (1995)]. Sequential resonance assignments of backbone ^{1}H, $.^{15}$ N, and $.^{13}$ C atoms may be made using a combination of triple resonance experiments similar to those previously described [Bagby et al., Biochemistry, 33:2409-2421 (1994a), except with enhanced sensitivity [Muhandiram and Kay, J. Magn. Reson., 103: 203-216 (1994), and minimal H_2O saturation [Kay et al., J. Magn. Reson., 109:129-133 (1994)]. Side chain ^{1}H and ^{13} C assignments may be made using HCCH-TOCSY [Bax et al., J. Magn. Reson., 87:620-627 (1990)] experiments with mixing times of 8 ms and 16 ms.in solution but need not be included in structure calculations. Nuclear Overhauser effect (NOE) cross peaks in

two-dimensional ^{1}H--^{1}H NOE spectroscopy (NOESY), three-dimensional ^{15}N-edited NOESY-HSQC [Zhang et al., J. Biomol, NMR, 4:845-858 (1994)] and three-dimensional simultaneous acquisition ^{15} N/^{13}C-edited NOE [Pascal et al., J. Magn. Reson., 103:197-201 (1994)], spectra may be obtained with 100 ms NOE mixing times. Standard pseudo-atom distance corrections [Wuthrich et al., J. Mol. Biol., 169:949-961 (1983)], may be incorporated to account for center averaging. An additional 0.5 .ANG. may be added to the upper limits for distances involving methyl groups [Wagner et al., J. Mol. Biol., 196:611-639 (1987); Clore et al., Biochemistry, 26:8012-8023 (1987)].

The structures can be calculated using a simulated annealing protocol [Nilges et al., In computational Aspects of the Study of Biological Macromolecules by Nuclear Magnetic Resonance Spectroscopy, J. C. Hoch, F. M. Poulsen, and C. Redfield, eds., New York: Plenum Press, pp. 451-455 (1991)], within X-PLOR [Brunger, X-PLOR Manual, Version 3.1, New Haven, Conn.: Department of Molecular Biophysics and Biochemistry, Yale University (1993)], using the previously described strategy [Bagby et al., Structure, 2:107-122 (1994b)]. Interhelical anges may be calculated using a program written by K. Yap. Accessible surface areas were calculated using the program Naccess, available from Prof. J. Thornton, University College, London.

Compounds capable of reducing the activity or amount of gene products required for cellular proliferation may be identified using the methods described in US Pat. No. 6,077,682. Briefly, the three-dimensional structure of the gene product or portion thereof may be used in a drug screening assay by (a) selecting a potential drug by performing rational drug design with the three-dimensional structure determined from one or more sets of atomic coordinates of the gene product or portion thereof in conjunction with computer modeling; (b) contacting the potential drug with a polypeptide comprising the gene product or portion thereof and (c) detecting the binding of the potential drug with said polypeptide; wherein a potential drug is selected as a drug if the potential drug binds to the polypeptide. In some methods, the three-dimensional structure of the gene product or portion thereof is used in a drug screening assay involving (a) selecting a potential drug by performing structural based rotational drug design with the three-dimensional structure of the gene product or portion thereof; wherein said selecting is performed in conjunction with computer modeling; (b) contacting the potential drug with a polypeptide comprising the gene product or portion thereof in the presence of a substrate of the gene product; wherein in the absence of the potential drug the substrate is acted upon by the gene product; and (c) determining the extent to which the gene product acted upon the substrate; wherein a drug is selected when a decrease in the action of the gene product on the substrate is determined in the presence of the potential drug relative to in its absence. In some

embodiments, the preceding method further involves(d) contacting the potential drug with the gene product or portion thereof for NMR analysis; wherein a binding complex forms between the potential drug and said gene product or portion thereof for NMR analysis; wherein the gene product or portion thereof for NMR analysis comprises a conservative amino acid substitution; (e) determining the three-dimensional structure of the binding complex by NMR; and (f) selecting a candidate drug by performing structural based rational drug design with the three-dimensional structure determined for the binding complex; wherein said selecting is performed in conjunction with computer modeling; (g) contacting the candidate drug with a second polypeptide comprising the gene product or portion thereof in the presence of a substrate of the gene product or portion thereof; wherein in the absence of the candidate drug the substrate is acted upon by the second polypeptide; and (h) determining the amount of action of the second polypeptide on the substrate; wherein a drug is selected when a decrease in the amount of action of the second polypeptide is determined in the presence of the candidate drug relative to in its absence.

Once the three-dimensional structure of a crystal comprising an essential gene product is determined, a potential modulator of its activity, can be examined through the use of computer modeling using a docking program such as FlexX, GRAM, DOCK, or AUTODOCK [Dunbrack et al., 1997, supra], to identify potential modulators. This procedure can include computer fitting of potential modulators to the polypeptide or fragments thereof to ascertain how well the shape and the chemical structure of the potential modulator will bind. Computer programs can also be employed to estimate the attraction, repulsion, and steric hindrance of the two binding partners (e.g., the essential gene product and a potential modulator). Generally the tighter the fit, the lower the steric hindrances, and the greater the attractive forces, the more potent the potential modulator since these properties are consistent with a tighter binding constant. Furthermore, the more specificity in the design of a potential drug the more likely that the drug will not interact as well with other proteins. This will minimize potential side-effects due to unwanted interactions with other proteins.

Compound and compound analogs can be systematically modified by computer modeling programs until one or more promising potential analogs is identified. In addition systematic modification of selected analogs can then be systematically modified by computer modeling programs until one or more potential analogs are identified. Such analysis has been shown to be effective in the development of HIV protease inhibitors [Lam et al., Science 263:380-384 (1994); Wlodawer et al., Ann. Rev. Biochem. 62:543-585 (1993); Appelt, Perspectives in Drug Discovery and Design 1:23-48 (1993); Erickson, Perspectives in Drug Discovery and Design 1:109-128 (1993)]. Alternatively a potential modulator could be

obtained by initially screening a random peptide library produced by recombinant bacteriophage for example, [Scott and Smith, Science, 249:386-390 (1990); Cwirla et al., Proc. Natl. Acad. Sci., 87:6378-6382 (1990); Devlin et al., Science, 249:404-406 (1990)]. A peptide selected in this manner would then be systematically modified by computer modeling programs as described above, and then treated analogously to a structural analog.

Example 91 describes computer modelling of the structures of gene products required for proliferation.

EXAMPLE 91

Determination of the Structure of Gene Products Required for Proliferation Using Computer Modelling

Three dimensional models were built by applying computer modelling methods to some of the gene products required for proliferation of *Staphylococcus aureus* using the amino acid sequences of the encoded proteins as follows. Sir Tom Blundell's program COMPOSER as provided by Tripos Associates in their BIOPOLYMER module to SYBYL was used to build the models. Skolnik's method of topology fingerprinting as implemented in Matchmaker was used to score the average mutation free energy. This number is in Boltzmans (units of kT) and should be negative (the more negative, the better the model.

Composer uses a Needleman Wunsch alignment with jumbling to find significant alignments. The reported parameters are percent identity and significance as measured from the jumbling. Those matches which were 30% identical and had a significance greater that 4 on the scale were judged to be good candidates for model building templates. If no three dimensional structures met these criteria, then a BLAST search was conducted against the most recent PDB sequence database. Any significant hits discovered in this manner were then added to the binary protein structure database and the candidate search was repeated in the manner discussed above.

In the next phase, Composer assigned structurally conserved and structurally variable regions and built the backbone structure and then searched the database for structures of the variable loops. These were then spliced in and a model of the protein resulted. Any loops (variable regions) which were unassignable were manually built and refined with a combination of dynamics.

The structure was then refined. Hydrogen atoms were added and a non-active aggregate was defined. 1000pS of dynamics using AMBER ALL-ATOM and Kollman charges are performed. Next a minimization cycle of up 5000 steepest decent steps were performed and then the aggregate was thawed and the process was repeated on the entire protein.

The resulting structure was then validated in MATCHMAKER. The topologicaly scanned free energy determined from empirically derived protein topologies was computed and the average energy/residue is reported in Boltzamans was reported. As this number represents a free energy the more negative it is the more favorable it is.

Sixty six proteins required for the proliferation of *Staphylococcus aureus* were modelled as described above. MATCHMAKER energies were computed for these. The distribution of the models built by class is shown in Table VIII below.

Table VIII: Distribution of models built with their MATCHMAKER energies in kT

Classification	Number of Models	Average Matchmaker Energy
Acylases	1	-0.10
Dehydrogenases	3	-0.12
DNA Related	3	-0.12
Heat Shock Protein	2	-0.16
Hydrolases	3	-0.16
Isomerases	1	0.05
Ligases	7	-0.07
Lyases	1	-0.09
Membrane Anchored	1	-0.12
Misc	18	-0.21
Oxidoreductases	6	-0.09
Proteases	1	-0.03
Ribosome	3	-0.11
Synthases	4	-0.14
Transferases	6	-0.12

The validity of the above method was confirmed using FtsZ. In the case of FtsZ, a crystal structure from M. Janeschi was available. Examination of the gross structural features determined using the above modelling showed all of the folds in the correct place, although there were some minor differences from the structure determined by x-ray crystallography.

EXAMPLE 92

Functional Complementation

In another embodiment, gene products whose activities may be complemented by a proliferation-required gene product from *Escherichia coli, Staphylococcus aureus, Enterococcus faecalis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella typhimurium, Acinetobacter baumannii, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Corynebacterium diptheriae, Enterobacter cloacae, Enterococcus faecium, Haemophilus influenzae, Helicobacter pylori, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis,*

Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Pasteurella multocida, Proteus mirabilis, Pseudomonas putida, Pseudomonas syringae, Salmonella paratyphi, Salmonella typhi, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae or *Yersinia pestis* or homologous polypeptides are identified using merodiploids, created by introducing a plasmid or Bacterial Artificial Chromosome into an organism having a mutation in the essential gene which reduces or eliminates the activity of the gene product. In some embodiments, the mutation may be a conditional mutation, such as a temperature sensitive mutation, such that the organism proliferates under permissive conditions but is unable to proliferate under non-permissive conditions in the absence of complementation by the gene on the plasmid or Bacterial Artificial Chromosome. Alternatively, duplications may be constructed as described in Roth et al. (1987) Biosynthesis of Aromatic Amino Acids in Escherichia coli and Salmonella typhimurium, F. C. ***Neidhardt,*** ed., American Society for Microbiology, publisher, pp. 2269-2270. Such methods are familiar to those skilled in the art.

It will be appreciated that no matter how detailed the foregoing appears in text, the invention can be practiced in many ways. As is also stated above, it should further be noted that the use of particular terminology when describing certain features or aspects of the present invention should not be taken to imply that the broadest reasonable meaning of such terminology is not intended, or that the terminology is being re-defined herein to be restricted to including any specific characteristics of the features or aspects of the invention with which that terminology is associated. Thus, although this invention has been described in terms of certain preferred embodiments, other embodiments which will be apparent to those of ordinary skill in the art in view of the disclosure herein are also within the scope of this invention. Accordingly, the scope of the invention is intended to be defined only by reference to the appended claims and any equivalents thereof.

WHAT IS CLAIMED IS:

1. A purified or isolated nucleic acid sequence comprising a nucleotide sequence consisting essentially of one of SEQ ID NOs: 1-6213, wherein expression of said nucleic acid inhibits proliferation of a cell.

2. The nucleic acid sequence of Claim 1, wherein said nucleotide sequence is complementary to at least a portion of a coding sequence of a gene whose expression is required for proliferation of a cell.

3. The nucleic acid of Claim 1, wherein said nucleic acid sequence is complementary to at least a portion of a nucleotide sequence of an RNA required for proliferation of a cell.

4. The nucleic acid of Claim 3, wherein said RNA is an RNA comprising a sequence of nucleotides encoding more than one gene product.

5. A purified or isolated nucleic acid comprising a fragment of one of SEQ ID NOs.: 1-6213, said fragment selected from the group consisting of fragments comprising at least 10, at least 20, at least 25, at least 30, at least 50 and more than 50 consecutive nucleotides of one of SEQ ID NOs: 1-6213.

6. The fragment of Claim 5, wherein said fragment is included in a nucleic acid obtained from an organism selected from the group consisting of *Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella*

sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

7. The fragment of Claim 5, wherein said fragment is included in a nucleic acid obtained from an organism other than *Escherichia coli.*

8. A vector comprising a promoter operably linked to the nucleic acid of any one of Claims 1-7.

9. The vector of Claim 8, wherein said promoter is active in a microorganism selected from the group consisting of *Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

10. A host cell containing the vector of Claim 8 or Claim 9.

11. A purified or isolated antisense nucleic acid comprising a nucleotide sequence complementary to at least a portion of an intragenic sequence, intergenic sequence, sequences spanning at least a portion of two or more genes, 5' noncoding region, or 3' noncoding region within an operon comprising a proliferation-required gene whose activity or expression is inhibited by an antisense nucleic acid comprising the nucleotide sequence of one of SEQ ID NOs.: 1-6213.

12. The purified or isolated antisense nucleic acid of Claim 11, wherein said antisense nucleic acid is complementary to a nucleic acid from an organism selected from the group consisting of *Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

13. The purified or isolated antisense nucleic acid of Claim 11, wherein said nucleotide sequence is complementary to a nucleotide sequence of a nucleic acid from an organism other than *E. coli*.

14. The purified or isolated antisense nucleic acid of Claim 11, wherein said proliferation-required gene comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397.

15. A purified or isolated nucleic acid comprising a nucleotide sequence having at least 70% identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, fragments comprising at least 25 consecutive nucleotides of SEQ ID NOs.: 1-6213, the nucleotide sequences complementary to SEQ ID NOs.: 1-6213 and the sequences complementary to fragments comprising at least 25 consecutive nucleotides of SEQ ID NOs.: 1-6213 as determined using BLASTN version 2.0 with the default parameters.

16. The purified or isolated nucleic acid of Claim 15, wherein said nucleic acid is obtained from an organism selected from the group consisting of *Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

17. The nucleic acid of Claim 15, wherein said nucleic acid is obtained from an organism other than *E. coli*.

18. A vector comprising a promoter operably linked to a nucleic acid encoding a polypeptide whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence of any one of SEQ ID NOs.: 1-6213.

19. The vector of Claim 18, wherein said nucleic acid encoding said polypeptide is obtained from an organism selected from the group consisting of *Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

20. The vector of Claim 18, wherein said nucleotide sequence encoding said polypeptide is obtained from an organism other than *E. coli*.

21. A host cell containing the vector of Claim 18.

22. The vector of Claim 18, wherein said polypeptide comprises a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 42398-78581.

23. The vector of Claim 18, wherein said promoter is operably linked to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397.

24. A purified or isolated polypeptide comprising a polypeptide whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence of any one of SEQ ID NOs.: 1-6213, or a fragment selected from the group consisting of fragments comprising at least 5, at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of one of the said polypeptides.

25. The polypeptide of Claim 24, wherein said polypeptide comprises an amino acid sequence of any one of SEQ ID NOs.: 42398-78581 or a fragment comprising at least 5, at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42398-78581.

26. The polypeptide of Claim 24, wherein said polypeptide is obtained from an organism selected from the group consisting of *Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio*

vulnificans, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

27. The polypeptide of Claim 24, wherein said polypeptide is obtained from an organism other than *E. coli*.

28. A purified or isolated polypeptide comprising a polypeptide having at least 25% amino acid identity to a polypeptide whose expression is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, or at least 25% amino acid identity to a fragment comprising at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of a polypeptide whose expression is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 as determined using FASTA version 3.0t78 with the default parameters.

29. The polypeptide of Claim 28, wherein said polypeptide has at least 25% identity to a polypeptide comprising one of SEQ ID NOs: 42398-78581 or at least 25% identity to a fragment comprising at least 5, at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of a polypeptide comprising one of SEQ ID NOs.: 42398-78581 as determined using FASTA version 3.0t78 with the default parameters.

30. The polypeptide of Claim 28, wherein said polypeptide is obtained from an organism selected from the group consisting of Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella

boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

31. The polypeptide of Claim 28, wherein said polypeptide is obtained from an organism other than *E. coli*.

32. An antibody capable of specifically binding the polypeptide of one of Claims 28-31.

33. A method of producing a polypeptide, comprising introducing a vector comprising a promoter operably linked to a nucleic acid comprising a nucleotide sequence encoding a polypeptide whose expression is inhibited by an antisense nucleic acid comprising one of SEQ ID NOs.: 1-6213 into a cell.

34. The method of Claim 33, further comprising the step of isolating said polypeptide.

35. The method of Claim 33, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42398-78581.

36. The method of Claim 33, wherein said nucleic acid encoding said polypeptide is obtained from an organism selected from the group consisting of *Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi,*

Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

37. The method of Claim 33, wherein said nucleic acid encoding said polypeptide is obtained from an organism other than *E. coli*.

38. The method of Claim 33, wherein said promoter is operably linked to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397.

39. A method of inhibiting proliferation of a cell in an individual comprising inhibiting the activity or reducing the amount of a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 or inhibiting the activity or reducing the amount of a nucleic acid encoding said gene product.

40. The method of Claim 39, wherein said method comprises inhibiting said activity or reducing said amount of a gene product in an organism selected from the group consisting of *Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella*

boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

41. The method of Claim 39, wherein said method comprises inhibiting said activity or reducing said amount of a gene product in an organism other than *E. coli*.

42. The method of Claim 39, wherein said gene product is present in an organism other than *E. coli*.

43. The method of Claim 39, wherein said gene product comprises a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 42398-78581.

44. A method for identifying a compound which influences the activity of a gene product required for proliferation, said gene product comprising a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, said method comprising:

contacting said gene product with a candidate compound; and

determining whether said compound influences the activity of said gene product.

45. The method of Claim 44, wherein said gene product is from an organism selected from the group consisting of Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis,

Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

46. The method of Claim 44, wherein said gene product is from an organism other than *E. coli*.

47. The method of Claim 44, wherein said gene product is a polypeptide and said activity is an enzymatic activity.

48. The method of Claim 44, wherein said gene product is a polypeptide and said activity is a carbon compound catabolism activity.

49. The method of Claim 44, wherein said gene product is a polypeptide and said activity is a biosynthetic activity.

50. The method of Claim 44, wherein said gene product is a polypeptide and said activity is a transporter activity.

51. The method of Claim 44, wherein said gene product is a polypeptide and said activity is a transcriptional activity.

52. The method of Claim 44, wherein said gene product is a polypeptide and said activity is a DNA replication activity.

53. The method of Claim 44, wherein said gene product is a polypeptide and said activity is a cell division activity.

54. The method of Claim 44, wherein said gene product is an RNA.

55. The method of Claim 44, wherein said gene product is a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42398-78581.

56. A compound identified using the method of Claim 44.

57. A method for identifying a compound or nucleic acid having the ability to reduce the activity or level of a gene product required for proliferation, said gene product comprising a gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, said method comprising:

(a) contacting a target gene or RNA encoding said gene product with a candidate compound or nucleic acid; and

(b) measuring an activity of said target.

58. The method of Claim 57, wherein said target gene or RNA is from an organism selected from the group consisting of Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

59. The method of Claim 57, wherein said target gene or RNA is from an organism other than *E. coli*.

60. The method of Claim 57, wherein said gene product is from an organism other than *E. coli*.

61. The method of Claim 57, wherein said target is a messenger RNA molecule and said activity is translation of said messenger RNA.

62. The method of Claim 57, wherein said target is a messenger RNA molecule and said activity is transcription of a gene encoding said messenger RNA.

63. The method of Claim 57, wherein said target is a gene and said activity is transcription of said gene.

64. The method of Claim 57, wherein said target is a nontranslated RNA and said activity is processing or folding of said nontranslated RNA or assembly of said nontranslated RNA into a protein/RNA complex.

65. The method of Claim 57, wherein said target is a messenger RNA molecule encoding a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42398-78581.

66. The method of Claim 57, wherein said target comprises a nucleic acid selected from the group consisting of SEQ ID NOS.: 6214-42397.

67. A compound or nucleic acid identified using the method of Claim 57.

68. A method for identifying a compound which reduces the activity or level of a gene product required for proliferation of a cell, wherein the activity or expression of said gene product is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, said method comprising the steps of:

(a) providing a sublethal level of an antisense nucleic acid comprising a nucleotide sequence complementary to a nucleic acid comprising a nucleotide sequence encoding said gene product in a cell to reduce the activity or amount of said gene product in said cell, thereby producing a sensitized cell;

(b) contacting said sensitized cell with a compound; and

(c) determining the degree to which said compound inhibits proliferation of said sensitized cell relative to a cell which does not contain said antisense nucleic acid.

69. The method of Claim 68, wherein said determining step comprises determining whether said compound inhibits the growth of said sensitized cell to a greater extent than said compound inhibits the growth of a nonsensitized cell.

70. The method of Claim 68, wherein said cell is a Gram positive bacterium.

71. The method of Claim 68, wherein said Gram positive bacterium is selected from the group consisting of *Staphylococcus* species, *Streptococcus* species, *Enterococcus* species, *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

72. The method of Claim 68, wherein said bacterium is *Staphylococcus aureus*.

73. The method of Claim 72, wherein said *Staphylococcus* species is coagulase negative.

74. The method of Claim 72, wherein said bacterium is selected from the group consisting of *Staphylococcus aureus* RN450 and *Staphylococcus aureus* RN4220.

75. The method of Claim 68, wherein said cell is an organism selected from the group consisting of Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia

cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

76. The method of Claim 68, wherein said cell is not an *E. coli* cell.

77. The method of Claim 68, wherein said gene product is from an organism other than *E. coli*.

78. The method of Claim 68, wherein said antisense nucleic acid is transcribed from an inducible promoter.

79. The method of Claim 68, further comprising the step of contacting said cell with a concentration of inducer which induces transcription of said antisense nucleic acid to a sublethal level.

80. The method of Claim 68, wherein growth inhibition is measured by monitoring optical density of a culture growth solution.

81. The method of Claim 68, wherein said gene product is a polypeptide.

82. The method of Claim 81, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42398-78581.

83. The method of Claim 68, wherein said gene product is an RNA.

84. The method of Claim 68, wherein nucleic acid encoding said gene product comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397.

85. A compound identified using the method of Claim 68.

86. A method for inhibiting cellular proliferation comprising introducing an effective amount of a compound with activity against a gene whose activity or expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 or a compound with activity against the product of said gene into a population of cells expressing said gene.

87. The method of Claim 86, wherein said compound is an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, or a proliferation-inhibiting portion thereof.

88. The method of Claim 86, wherein said proliferation inhibiting portion of one of SEQ ID NOs.: 1-6213 is a fragment comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 51 consecutive nucleotides of one of SEQ ID NOs.: 1-6213.

89. The method of Claim 86, wherein said population is a population of Gram positive bacteria.

90. The method of Claim 89, wherein said population of Gram positive bacteria is selected from the group consisting of a population of *Staphylococcus* species, *Streptococcus* species, *Enterococcus* species, *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

91. The method of Claim 86, wherein said population is a population of *Staphylococcus aureus*.

92. The method of Claim 91, wherein said population is a population of a bacterium selected from the group consisting of *Staphylococcus aureus* RN450 and *Staphylococcus aureus* RN4220.

93. The method of Claim 86, wherein said population is a population of a bacterium selected from the group consisting of Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae,

Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

94. The method of Claim 86, wherein said population is a population of an organism other than *E. coli*.

95. The method of Claim 86, wherein said product of said gene is from an organism other than *E. coli*.

96. The method of Claim 86, wherein said gene encodes a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42398-78581.

97. The method of Claim 86, wherein said gene comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397.

98. A composition comprising an effective concentration of an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, or a proliferation-inhibiting portion thereof in a pharmaceutically acceptable carrier.

99. The composition of Claim 98, wherein said proliferation-inhibiting portion of one of SEQ ID NOs.: 1-6213 comprises at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive nucleotides of one of SEQ ID NOs.: 1-6213.

100. A method for inhibiting the activity or expression of a gene in an operon required for proliferation wherein the activity or expression of at least one gene in said operon is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-6213, said method comprising contacting a cell in a cell population with an antisense nucleic acid complementary to at least a portion of said operon.

101. The method of Claim 100, wherein said antisense nucleic acid comprises a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 or a proliferation-inhibiting portion thereof.

102. The method of Claim 100, wherein said cell is selected from the group consisting of Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

103. The method of Claim 100, wherein said cell is not an *E. coli* cell.

104. The method of Claim 100, wherein said gene is from an organism other than *E. coli*.

105. The method of Claim 100, wherein said cell is contacted with said antisense nucleic acid by introducing a plasmid which expresses said antisense nucleic acid into said cell population.

106. The method of Claim 100, wherein said cell is contacted with said antisense nucleic acid by introducing a phage which encodes said antisense nucleic acid into said cell population.

107. The method of Claim 100, wherein said cell is contacted with said antisense nucleic acid by expressing said antisense nucleic acid from the chromosome of cells in said cell population.

108. The method of Claim 100, wherein said cell is contacted with said antisense nucleic acid by introducing a promoter adjacent to a chromosomal copy of said antisense nucleic acid such that said promoter directs the transcription of said antisense nucleic acid.

109. The method of Claim 100, wherein said cell is contacted with said antisense nucleic acid by introducing a retron which expresses said antisense nucleic acid into said cell population.

110. The method of Claim 100, wherein said cell is contacted with said antisense nucleic acid by introducing a ribozyme into said cell-population, wherein a binding portion of said ribozyme comprises said antisense nucleic acid.

111. The method of Claim 100, wherein said cell is contacted with said antisense nucleic acid by introducing a liposome comprising said antisense nucleic acid into said cell.

112. The method of Claim 100, wherein said cell is contacted with said antisense nucleic acid by electroporation of said antisense nucleic acid into said cell.

113. The method of Claim 100, wherein said antisense nucleic acid is a fragment comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive nucleotides of one of SEQ ID NOs.: 1-6213.

114. The method of Claim 100 wherein said antisense nucleic acid is a synthetic oligonucleotide.

115. The method of Claim 100, wherein said gene comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397.

116. A method for identifying a gene which is required for proliferation of a cell comprising:

(a) contacting a cell with an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, wherein said cell is a cell other than the organism from which said nucleic acid was obtained;

(b) determining whether said nucleic acid inhibits proliferation of said cell; and

(c) identifying the gene in said cell which encodes the mRNA which is complementary to said antisense nucleic acid or a portion thereof.

117. The method of Claim 116, wherein said cell is selected from the group consisting of *Staphylococcus* species, *Streptococcus* species, *Enterococcus* species, *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

118. The method of Claim 116 wherein said cell is selected from the group consisting of Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

119. The method of Claim 116, wherein said cell is not *E. coli*.

120. The method of Claim 116, further comprising operably linking said antisense nucleic acid to a promoter which is functional in said cell, said promoter being included in a vector, and introducing said vector into said cell.

121. A method for identifying a compound having the ability to inhibit proliferation of a cell comprising:

(a) identifying a homolog of a gene or gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs. 1-6213 in a test cell, wherein said test cell is not the cell from which said nucleic acid was obtained;

(b) identifying an inhibitory nucleic acid sequence which inhibits the activity of said homolog in said test cell;

(c) contacting said test cell with a sublethal level of said inhibitory nucleic acid, thus sensitizing said cell;

(d) contacting the sensitized cell of step (c) with a compound; and

(e) determining the degree to which said compound inhibits proliferation of said sensitized cell relative to a cell which does not contain said inhibitory nucleic acid.

122. The method of Claim 121, wherein said determining step comprises determining whether said compound inhibits proliferation of said sensitized test cell to a greater extent than said compound inhibits proliferation of a nonsensitized test cell.

123. The method of Claim 121, wherein step (a) comprises identifying a nucleic acid homologous to a gene or gene product whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs. 1-6213 or a nucleic acid encoding a homologous polypeptide to a polypeptide whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs. 1-6213 by using an algorithm selected from the group consisting of BLASTN version 2.0 with the default parameters and FASTA version 3.0t78 algorithm with the default parameters to identify said homologous nucleic acid or said nucleic acid encoding a homologous polypeptide in a database.

124. The method of Claim 121 wherein said step (a) comprises identifying a homologous nucleic acid or a nucleic acid comprising a sequence of nucleotides encoding a homologous polypeptide by identifying nucleic acids which hybridize to said nucleic acid selected from the group consisting of SEQ ID NOs. 1-6213 or the complement of said nucleic acid selected from the group consisting of SEQ ID NOs. 1-6213.

125. The method of Claim 121 wherein step (a) comprises expressing a nucleic acid selected from the group consisting of SEQ ID NOs. 1-6213 in said test cell.

126. The method of Claim 121, wherein step (a) comprises identifying a homologous nucleic acid or a nucleic acid encoding a homologous polypeptide in a test cell selected from the group consisting of *Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum,*

Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

127. The method of Claim 121, wherein step (a) comprises identifying a homologous nucleic acid or a nucleic acid encoding a homologous polypeptide in a test cell other than *E. coli*.

128. The method of Claim 121, wherein said inhibitory nucleic acid is an antisense nucleic acid.

129. The method of Claim 121, wherein said inhibitory nucleic acid comprises an antisense nucleic acid to a portion of said homolog.

130. The method of Claim 121, wherein said inhibitory nucleic acid comprises an antisense nucleic acid to a portion of the operon encoding said homolog.

131. The method of Claim 121, wherein the step of contacting the cell with a sublethal level of said inhibitory nucleic acid comprises directly contacting the surface of said cell with said inhibitory nucleic acid.

132. The method of Claim 121, wherein the step of contacting the cell with a sublethal level of said inhibitory nucleic acid comprises transcribing an antisense nucleic acid complementary to at least a portion of the RNA transcribed from said homolog in said cell.

133. The method of Claim 121, wherein said gene product comprises a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42398-78581.

134. The method of Claim 121, wherein said gene comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397.

135. A compound identified using the method of Claim 121.

136. A method of identifying a compound having the ability to inhibit proliferation comprising:

(a) contacting a test cell with a sublethal level of a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs. 1-6213 or a portion thereof which inhibits the proliferation of the cell from which said nucleic acid was obtained, thus sensitizing said test cell;

(b) contacting the sensitized test cell of step (a) with a compound; and

(c) determining the degree to which said compound inhibits proliferation of said sensitized test cell relative to a cell which does not contain said nucleic acid.

137. The method of Claim 136, wherein said determining step comprises determining whether said compound inhibits proliferation of said sensitized test cell to a greater extent than said compound inhibits proliferation of a nonsensitized test cell.

138. A compound identified using the method of Claim 136.

139. The method of Claim 136, wherein said test cell is selected from the group consisting of Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio

vulnificans, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

140. The method of Claim 136, wherein the test cell is not *E. coli.*

141. A method for identifying a compound having activity against a biological pathway required for proliferation comprising:

(a) sensitizing a cell by providing a sublethal level of an antisense nucleic acid complementary to a nucleic acid encoding a gene product required for proliferation, wherein the activity or expression of said gene product is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, in said cell to reduce the activity or amount of said gene product;

(b) contacting the sensitized cell with a compound; and

(c) determining the degree to which said compound inhibits the growth of said sensitized cell relative to a cell which does not contain said antisense nucleic acid.

142. The method of Claim 141, wherein said determining step comprises determining whether said compound inhibits the growth of said sensitized cell to a greater extent than said compound inhibits the growth of a nonsensitized cell.

143. The method of Claim 141, wherein said cell is selected from the group consisting of bacterial cells, fungal cells, plant cells, and animal cells.

144. The method of Claim 141, wherein said cell is a Gram positive bacterium.

145. The method of Claim 144, wherein said Gram positive bacterium is selected from the group consisting of *Staphylococcus* species, *Streptococcus* species, *Enterococcus* species, *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

146. The method of Claim 145, wherein said Gram positive bacterium is *Staphylococcus aureus*.

147. The method of Claim 146, wherein said Gram positive bacterium is selected from the group consisting of *Staphylococcus aureus* RN450 and *Staphylococcus aureus* RN4220.

148. The method of Claim 141, wherein said cell is selected from the group consisting of Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum,

Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

149. The method of Claim 141, wherein said cell is not an *E. coli* cell.

150. The method of Claim 141, wherein said gene product is from an organism other than *E. coli*.

151. The method of Claim 141, wherein said antisense nucleic acid is transcribed from an inducible promoter.

152. The method of Claim 141, further comprising contacting the cell with an agent which induces transcription of said antisense nucleic acid from said inducible promoter, wherein said antisense nucleic acid is transcribed at a sublethal level.

153. The method of Claim 141, wherein inhibition of proliferation is measured by monitoring the optical density of a liquid culture.

154. The method of Claim 141, wherein said gene product comprises a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42398-78581.

155. The method of Claim 141, wherein said nucleic acid encoding said gene product comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397.

156. A compound identified using the method of Claim 141.

157. A method for identifying a compound having the ability to inhibit cellular proliferation comprising:

(a) contacting a cell with an agent which reduces the activity or level of a gene product required for proliferation of said cell, wherein said gene product is a gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213;

(b) contacting said cell with a compound; and

(c) determining whether said compound reduces proliferation of said contacted cell by acting on said gene product.

158. The method of Claim 157, wherein said determining step comprises determining whether said compound reduces proliferation of said contacted cell to a greater extent than said compound reduces proliferation of cells which have not been contacted with said agent.

159. The method of Claim 157, wherein said cell is selected from the group consisting of Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

160. The method of Claim 157, wherein said cell is not an *E. coli* cell.

161. The method of Claim 157, wherein said gene product is from an organism other than *E. coli*.

162. The method of Claim 157, wherein said agent which reduces the activity or level of a gene product required for proliferation of said cell comprises an antisense nucleic acid to a gene or operon required for proliferation.

163. The method of Claim 157, wherein said agent which reduces the activity or level of a gene product required for proliferation of said cell comprises a compound known to inhibit growth or proliferation of a cell.

164. The method of Claim 157, wherein said cell contains a mutation which reduces the activity or level of said gene product required for proliferation of said cell.

165. The method of Claim 157, wherein said mutation is a temperature sensitive mutation.

166. The method of Claim 157, wherein said gene product comprises a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42398-78581.

167. A compound identified using the method of Claim 157.

168. A method for identifying the biological pathway in which a proliferation-required gene or its gene product lies, wherein said gene or gene product comprises a gene or gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-6213, said method comprising:

(a) providing a sublethal level of an antisense nucleic acid which inhibits the activity of said proliferation-required gene or gene product in a test cell;

(b) contacting said test cell with a compound known to inhibit growth or proliferation of a cell, wherein the biological pathway on which said compound acts is known; and

(c) determining the degree to which said proliferation of said test cell is inhibited relative to a cell which was not contacted with said compound.

169. The method of Claim 168, wherein said determining step comprises determining whether said test cell has a substantially greater sensitivity to said compound than a cell which does not express said sublethal level of said antisense nucleic acid.

170. The method of Claim 168, wherein said gene product comprises a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42398-78581.

171. The method of Claim 168, wherein said test cell is selected from the group consisting of Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

172. The method of Claim 168, wherein said test cell is not an *E. coli* cell.

173. The method of Claim 168, wherein said gene product is from an organism other than *E. coli*.

174. A method for determining the biological pathway on which a test compound acts comprising:

(a) providing a sublethal level of an antisense nucleic acid complementary to a proliferation-required nucleic acid in a first cell, wherein the activity or expression of said proliferation-required nucleic acid is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-6213 and wherein the biological pathway in which said proliferation-required nucleic acid or a protein encoded by said proliferation-required nucleic acid lies is known,

(b) contacting said first cell with said test compound; and

(c) determining the degree to which said test compound inhibits proliferation of said first cell relative to a cell which does not contain said antisense nucleic acid.

175. The method of Claim 174, wherein said determining step comprises determining whether said first cell has a substantially greater sensitivity to said test compound than a cell which does not express said sublethal level of said antisense nucleic acid.

176. The method of Claim 174, further comprising:

(d) providing a sublethal level of a second antisense nucleic acid complementary to a second proliferation-required nucleic acid in a second cell, wherein said second proliferation-required nucleic acid is in a different biological pathway than said proliferation-required nucleic acid in step (a); and

(e) determining whether said second cell does not have a substantially greater sensitivity to said test compound than a cell which does not express said sublethal level of said second antisense nucleic acid, wherein said test compound is specific for the biological pathway against which the antisense nucleic acid of step (a) acts if said first cell has a substantially greater sensitivity to said test compound than said second cell.

177. The method of Claim 174, wherein said first cell is selected from the group consisting of Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema

pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

178. The method of Claim 174, wherein said first cell is not an *E. coli* cell.

179. The method of Claim 174, wherein said proliferation-required nucleic acid is from an organism other than *E. coli*.

180. A purified or isolated nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-6213.

181. A compound which interacts with a gene or gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence of one of SEQ ID NOs.: 1-6213 to inhibit proliferation.

182. The compound of Claim 181, wherein said gene product is a polypeptide comprising one of SEQ ID NOs.: 42398-78581.

183. The compound of Claim 181, wherein said gene comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397.

184. A compound which interacts with a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence of one of SEQ ID NOs.: 1-6213 to inhibit proliferation.

185. A method for manufacturing an antibiotic comprising the steps of:

screening one or more candidate compounds to identify a compound that reduces the activity or level of a gene product required for proliferation, said gene product comprising a gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213; and

manufacturing the compound so identified.

186. The method of Claim 185, wherein said screening step comprises performing any one of the methods of Claims 44, 68, 121, 136, 141, and 157.

187. The method of Claim 185, wherein said gene product is a polypeptide comprising one of SEQ ID NOs:42398-78581.

188. A method for inhibiting proliferation of a cell in a subject comprising administering an effective amount of a compound that reduces the activity or level of a gene product required for proliferation of said cell, said gene product comprising a gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 to said subject.

189. The method of Claim 188 wherein said subject is selected from the group consisting of vertebrates, mammals, avians, and human beings.

190. The method of Claim 188, wherein said gene product comprises a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42398-78581.

191. The method of Claim 188, wherein said cell is selected from the group consisting of Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

192. The method of Claim 188, wherein said cell is not *E. coli*.

193. The method of Claim 188, wherein said gene product is from an organism other than *E. coli*.

194. A purified or isolated nucleic acid consisting essentially of the coding sequence of one of SEQ ID NOs: 6214-42397.

195. A fragment of the nucleic acid of Claim 8, said fragment comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive nucleotides of one of SEQ ID NOs: 6214-42397.

196. A purified or isolated nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397, fragments comprising at least 25 consecutive nucleotides of SEQ ID NOs.: 6214-42397, the nucleotide sequences complementary to SEQ ID NOs.:6214-42397, and the nucleotide sequences complementary to fragments comprising at least 25 consecutive nucleotides of SEQ ID NOs.: 6214-42397 as determined using BLASTN version 2.0 with the default parameters.

197. The nucleic acid of Claim 196, wherein said nucleic acid is from an organism selected from the group consisting of Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

198. The nucleic acid of Claim 196, wherein said nucleic acid is from an organism other than *E. coli*.

199. A method of inhibiting proliferation of a cell comprising inhibiting the activity or reducing the amount of a gene product in said cell or inhibiting the activity or reducing the amount of a nucleic acid encoding said gene product in said cell, wherein said gene product is

selected from the group consisting of a gene product having having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213.

200. The method of Claim 199, wherein said method comprises inhibiting said activity or reducing said amount of said gene product or inhibiting the activity or reducing the amount of a nucleic acid encoding said gene product in an organism selected from the group consisting of *Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida,*

Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

201. The method of Claim 199, wherein said method comprises inhibiting said activity or reducing said amount of said gene product or inhibiting the activity or reducing the amount of a nucleic acid encoding said gene product in an organism other than *E. coli*.

202. The method of Claim 199, wherein said gene product is from an organism other than *E. coli*.

203. The method of Claim 199, wherein said gene product comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 42398-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 42398-78581.

204. The method of Claim 199, wherein said gene product is encoded by a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid comprising a nucloetide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate condtions.

205. A method for identifying a compound which influences the activity of a gene product required for proliferation comprising:

contacting a candidate compound with a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as

determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 1-6213; and

determining whether said candidate compound influences the activity of said gene product.

206. The method of Claim 205, wherein said gene product is from an organism selected from the group consisting of Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus,

Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

207. The method of Claim 205, wherein said gene product is from an organism other than *E. coli*.

208. The method of Claim 205, wherein said gene product is a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 42398-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 42398-78581.

209. The method of Claim 205, wherein said gene product is encoded by a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate condtions.

210. A compound identified using the method of Claim 205.

211. A method for identifying a compound or nucleic acid having the ability to reduce the activity or level of a gene product required for proliferation comprising:

(a) providing a target that is a gene or RNA, wherein said target comprises a nucleic acid that encodes a gene product selected from the group consisting of a gene product having having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleic acid identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product

encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 1-6213;

(b) contacting said target with a candidate compound or nucleic acid; and

(c) measuring an activity of said target.

212. The method of Claim 211, wherein said target gene or RNA is from an organism selected from the group consisting of Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

213. The method of Claim 211, wherein said target gene or RNA is from an organism other than *E. coli*.

214. The method of Claim 211, wherein said gene product is from an organism other than *E. coli*.

215. The method of Claim 211, wherein said target is a messenger RNA molecule and said activity is translation of said messenger RNA.

216. The method of Claim 211, wherein said compound is a nucleic acid and said activity is translation of said gene product.

217. The method of Claim 211, wherein said target is a gene and said activity is transcription of said gene.

218. The method of Claim 211, wherein said target is a nontranslated RNA and said activity is processing or folding of said nontranslated RNA or assembly of said nontranslated RNA into a protein/RNA complex.

219. The method of Claim 211, wherein said target gene is a messenger RNA molecule encoding a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 42398-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 42398-78581.

220. The method of Claim 11, wherein said target gene comprises a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate condtions.

221. A compound or nucleic acid identified using the method of Claim 211.

222. A method for identifying a compound which reduces the activity or level of a gene product required for proliferation of a cell comprising:

(a) providing a sublethal level of an antisense nucleic acid complementary to a nucleic acid encoding said gene product in a cell to reduce the activity or amount of said gene product in said cell, thereby producing a sensitized cell, wherein said gene product is selected from the group consisting of a gene product having having at least 70% nucleic acid identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.:

1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 1-6213;

(b) contacting said sensitized cell with a compound; and

(c) determining the degree to which said compound inhibits the growth of said sensitized cell relative to a cell which does not contain said antisense nucleic acid.

223. The method of Claim 222, wherein said determining step comprises determining whether said compound inhibits the growth of said sensitized cell to a greater extent than said compound inhibits the growth of a nonsensitized cell.

224. The method of Claim 222, wherein said sensitized cell is a Gram positive bacterium.

225. The method of Claim 224, wherein said Gram positive bacterium is selected from the group consisting of *Staphylococcus* species, *Streptococcus* species, *Enterococcus* species, *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

226. The method of Claim 225, wherein said bacterium is *Staphylococcus aureus*.

227. The method of Claim 224, wherein said *Staphylococcus* species is coagulase negative.

228. The method of Claim 226, wherein said bacterium is selected from the group consisting of *Staphylococcus aureus* RN450 and *Staphylococcus aureus* RN4220.

229. The method of Claim 222, wherein said sensitized cell is an organism selected from the group consisting of Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni,

Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

230. The method of Claim 222, wherein said cell is an organism other than *E. coli*.

231. The method of Claim 222, wherein said gene product is from an organism other than *E. coli*.

232. The method of Claim 222, wherein said antisense nucleic acid is transcribed from an inducible promoter.

233. The method of Claim 222, further comprising the step of contacting said cell with a concentration of inducer which induces transcription of said antisense nucleic acid to a sublethal level.

234. The method of Claim 222, wherein growth inhibition is measured by monitoring optical density of a culture medium.

235. The method of Claim 222, wherein said gene product is a polypeptide.

236. The method of Claim 235, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 42398-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 42398-78581.

237. The method of Claim 222, wherein said gene product is an RNA.

238. The method of Claim 222, wherein said nucleic acid encoding said gene product comprises a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleic acid identity as determined using BLASTN version 2.0 with the default parameters to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate condtions.

239. A compound identified using the method of Claim 222.

240. A method for inhibiting cellular proliferation comprising introducing a compound with activity against a gene product or a compound with activity against a gene encoding said gene product into a population of cells expressing said gene product, wherein said gene product is selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 1-6213.

241. The method of Claim 240, wherein said compound is an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, or a proliferation-inhibiting portion thereof.

242. The method of Claim 240, wherein said proliferation inhibiting portion of one of SEQ ID NOs.: 1-6213 is a fragment comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 51 consecutive nucleotides of one of SEQ ID NOs.: 1-6213.

243. The method of Claim 240, wherein said population is a population of Gram positive bacteria.

244. The method of Claim 243, wherein said population of Gram positive bacteria is selected from the group consisting of a population of *Staphylococcus* species, *Streptococcus* species, *Enterococcus* species, *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

245. The method of Claim 243, wherein said population is a population of *Staphylococcus aureus*.

246. The method of Claim 245, wherein said population is a population of a bacterium selected from the group consisting of *Staphylococcus aureus* RN450 and *Staphylococcus aureus* RN4220.

247. The method of Claim 240, wherein said population is a population of a bacterium selected from the group consisting of Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum,

Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

248. The method of Claim 240, wherein said population is a population of an organism other than *E. coli*.

249. The method of Claim 240, wherein said product of said gene is from an organism other than *E. coli*.

250. The method of Claim 240, wherein said gene product is selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 42398-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 42398-78581.

251. The method of Claim 240, wherein said gene comprises a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate condtions.

252. A preparation comprising an effective concentration of an antisense nucleic acid in a pharmaceutically acceptable carrier wherein said antisense nucleic acid is selected from the group consisting of a nucleic acid comprising a sequence having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 or a proliferation-inhibiting portion thereof, a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions.

253. The preparation of Claim 252, wherein said proliferation-inhibiting portion of one of SEQ ID NOs.: 1-6213 comprises at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive nucleotides of one of SEQ ID NOs.: 1-6213.

254. A method for inhibiting the activity or expression of a gene in an operon which encodes a gene product required for proliferation comprising contacting a cell in a cell

population with an antisense nucleic acid comprising at least a proliferation-inhibiting portion of said operon in an antisense orientation, wherein said gene product is selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 1-6213.

255. The method of Claim 254, wherein said antisense nucleic acid comprises a nucleotide sequence having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide seqence selected from the group consisting of SEQ ID NOs.: 1-6213, a proliferation inhibiting portion thereof, a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, and a nucleic acid which comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions.

256. The method of Claim 254, wherein said cell is selected from the group consisting of Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis,

Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

257. The method of Claim 254, wherein said cell is not an *E. coli* cell.

258. The method of Claim 254, wherein said gene is from an organism other than *E. coli.*

259. The method of Claim 254, wherein said cell is contacted with said antisense nucleic acid by introducing a plasmid which transcribes said antisense nucleic acid into said cell population.

260. The method of Claim 254, wherein said cell is contacted with said antisense nucleic acid by introducing a phage which transcribes said antisense nucleic acid into said cell population.

261. The method of Claim 254, wherein said cell is contacted with said antisense nucleic acid by transcribing said antisense nucleic acid from the chromosome of cells in said cell population.

262. The method of Claim 254, wherein said cell is contacted with said antisense nucleic acid by introducing a promoter adjacent to a chromosomal copy of said antisense nucleic acid such that said promoter directs the synthesis of said antisense nucleic acid.

263. The method of Claim 254, wherein said cell is contacted with said antisense nucleic acid by introducing a retron which expresses said antisense nucleic acid into said cell population.

264. The method of Claim 254, wherein said cell is contacted with said antisense nucleic acid by introducing a ribozyme into said cell-population, wherein a binding portion of said ribozyme is complementary to said antisense oligonucleotide.

265. The method of Claim 254, wherein said cell is contacted with said antisense nucleic acid by introducing a liposome comprising said antisense oligonucleotide into said cell.

266. The method of Claim 254, wherein said cell is contacted with said antisense nucleic acid by electroporation of said antisense nucleic acid into said cell.

267. The method of Claim 254, wherein said antisense nucleic acid has at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive nucleotides of one of SEQ ID NOs.: 1-6213.

268. The method of Claim 254 wherein said antisense nucleic acid is a synthetic oligonucleotide.

269. The method of Claim 254, wherein said gene comprises a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate condtions.

270. A method for identifying a gene which is required for proliferation of a cell comprising:

(a) contacting a cell with an antisense nucleic acid selected from the group consisting of a nucleic acid at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 or a proliferation-inhibiting portion thereof, a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, wherein said cell is a cell other than the organism from which said nucleic acid was obtained;

(b) determining whether said nucleic acid inhibits proliferation of said cell; and

(c) identifying the gene in said cell which encodes the mRNA which is complementary to said antisense nucleic acid or a portion thereof.

271. The method of Claim 270, wherein said cell is selected from the group consisting of *Staphylococcus* species, *Streptococcus* species, *Enterococcus* species, *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

272. The method of Claim 270 wherein said cell is selected from the group consisting of Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

273. The method of Claim 270, wherein said cell is not *E. coli*.

274. The method of Claim 270, further comprising operably linking said antisense nucleic acid to a promoter which is functional in said cell, said promoter being included in a vector, and introducing said vector into said cell.

275. A method for identifying a compound having the ability to inhibit proliferation of a cell comprising:

(a) identifying a homolog of a gene or gene product whose activity or level is inhibited by an antisense nucleic acid in a test cell, wherein said test cell is not the microorgaism from which the antisense nucleic acid was obtained, wherein said antisense nucleic acid is selected from the group consisting of a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOs. 1-6213, a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions;

(b) identifying an inhibitory nucleic acid sequence which inhibits the activity of said homolog in said test cell;

(c) contacting said test cell with a sublethal level of said inhibitory nucleic acid, thus sensitizing said cell;

(d) contacting the sensitized cell of step (c) with a compound; and

(e) determining the degree to which said compound inhibits proliferation of said sensitized cell relative to a cell which does not express said inhibitory nucleic acid.

276. The method of Claim 275, wherein said determining step comprises determining whether said compound inhibits proliferation of said sensitized test cell to a greater extent than said compound inhibits proliferation of a nonsensitized test cell.

277. The method of Claim 275, wherein step (a) comprises identifying a homologous nucleic acid to a gene or gene product whose activity or level is inhibited by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOs. 1-6213 or a nucleic acid encoding a homologous polypeptide to a polypeptide whose activity or level is inhibited by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOs. 1-6213 by using an algorithm selected from the group consisting of BLASTN version 2.0 with the default parameters and FASTA version 3.0t78 algorithm with the default parameters to identify said homologous nucleic acid or said nucleic acid encoding a homologous polypeptide in a database.

278. The method of Claim 275 wherein said step (a) comprises identifying a homologous nucleic acid or a nucleic acid encoding a homologous polypeptide by identifying nucleic acids comprising nucleotide sequences which hybridize to said nucleic acid having at

least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOs. 1-6213 or the complement of the nucleotide sequence of said nucleic acid selected from the group consisting of SEQ ID NOs. 1-6213.

279. The method of Claim 275 wherein step (a) comprises expressing a nucleic acid having at least 70% nucleic acid identity as determined using BLASTN version 2.0 with the default parameters to a sequence selected from the group consisting of SEQ ID NOs. 1-6213 in said test cell.

280. The method of Claim 275, wherein step (a) comprises identifying a homologous nucleic acid or a nucleic acid encoding a homologous polypeptide in an test cell selected from the group consisting of *Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

281. The method of Claim 275, wherein step (a) comprises identifying a homologous nucleic acid or a nucleic acid encoding a homologous polypeptide in a test cell other than *E. coli*.

282. The method of Claim 275, wherein said inhibitory nucleic acid is an antisense nucleic acid.

283. The method of Claim 275, wherein said inhibitory nucleic acid comprises an antisense nucleic acid to a portion of said homolog.

284. The method of Claim 275, wherein said inhibitory nucleic acid comprises an antisense nucleic acid to a portion of the operon encoding said homolog.

285. The method of Claim 275, wherein the step of contacting the cell with a sublethal level of said inhibitory nucleic acid comprises directly contacting said cell with said inhibitory nucleic acid.

286. The method of Claim 275, wherein the step of contacting the cell with a sublethal level of said inhibitory nucleic acid comprises expressing an antisense nucleic acid to said homolog in said cell.

287. The method of Claim 275, wherein said gene product comprises a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42398-78581.

288. The method of Claim 275, wherein said gene comprises a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate condtions.

289. A compound identified using the method of Claim 275.

290. A method of identifying a compound having the ability to inhibit proliferation comprising:

(a) sensitizing a test cell by contacting said test cell with a sublethal level of an antisense nucleic acid, wherein said antisense nucleic acid is selected from the group consisting of a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOs. 1-6213 or a portion thereof which inhibits the proliferation of the cell from which said nucleic acid was

obtained, a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditionst;

(b) contacting the sensitized test cell of step (a) with a compound; and

(c) determining the degree to which said compound inhibits proliferation of said sensitized test cell relative to a cell which does not contain said antisense nucleic acid.

291. The method of Claim 290, wherein said determining step comprises determining whether said compound inhibits proliferation of said sensitized test cell to a greater extent than said compound inhibits proliferation of a nonsensitized test cell.

292. A compound identified using the method of Claim 290.

293. The method of Claim 290, wherein said test cell is selected from the group consisting of Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio

vulnificans, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

294. The method of Claim 290, wherein the test cell is not *E. coli*.

295. A method for identifying a compound having activity against a biological pathway required for proliferation comprising:

(a) sensitizing a cell by providing a sublethal level of an antisense nucleic acid complementary to a nucleic acid encoding a gene product required for proliferation, wherein said gene product is selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 1-6213;

(b) contacting the sensitized cell with a compound; and

(c) determining the extent to which said compound inhibits the growth of said sensitized cell relative to a cell which does not contain said antisense nucleic acid.

296. The method of Claim 295, wherein said determining step comprises determining whether said compound inhibits the growth of said sensitized cell to a greater extent than said compound inhibits the growth of a nonsensitized cell.

297. The method of Claim 295, wherein said cell is selected from the group consisting of bacterial cells, fungal cells, plant cells, and animal cells.

298. The method of Claim 295, wherein said cell is a Gram positive bacterium.

299. The method of Claim 298, wherein said Gram positive bacterium is selected from the group consisting of *Staphylococcus* species, *Streptococcus* species, *Enterococcus* species, *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

300. The method of Claim 299, wherein said Gram positive bacterium is *Staphylococcus aureus*.

301. The method of Claim 298, wherein said Gram positive bacterium is selected from the group consisting of *Staphylococcus aureus* RN450 and *Staphylococcus aureus* RN4220.

302. The method of Claim 295, wherein said cell is selected from the group consisting of Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

303. The method of Claim 295, wherein said cell is not an *E. coli* cell.

304. The method of Claim 295, wherein said gene product is from an organism other than *E. coli*.

305. The method of Claim 295, wherein said antisense nucleic acid is transcribed from an inducible promoter.

306. The method of Claim 305, further comprising contacting the cell with an agent which induces expression of said antisense nucleic acid from said inducible promoter, wherein said antisense nucleic acid is expressed at a sublethal level.

307. The method of Claim 295, wherein inhibition of proliferation is measured by monitoring the optical density of a liquid culture.

308. The method of Claim 295, wherein said gene product comprises a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a sequence selected from the group consisting of SEQ ID NOs.: 42398-78581.

309. The method of Claim 295, wherein said nucleic acid encoding said gene product comprises a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate condtions.

310. A compound identified using the method of Claim 295.

311. A method for identifying a compound having the ability to inhibit cellular proliferation comprising:

(a) contacting a cell with an agent which reduces the activity or level of a gene product required for proliferation of said cell, wherein said gene product is selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product

whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 1-6213;

(b) contacting said cell with a compound; and

(c) determining the degree to which said compound reduces proliferation of said contacted cell relative to a cell which was not contacted with said agent.

312. The method of Claim 311, wherein said determining step comprises determining whether said compound reduces proliferation of said contacted cell to a greater extent than said compound reduces proliferation of cells which have not been contacted with said agent.

313. The method of Claim 311, wherein said cell is selected from the group consisting of Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus,

Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

314. The method of Claim 311, wherein said cell is not an *E. coli* cell.

315. The method of Claim 311, wherein said gene product is from an organism other than *E. coli*.

316. The method of Claim 311, wherein said agent which reduces the activity or level of a gene product required for proliferation of said cell comprises an antisense nucleic acid to a gene or operon required for proliferation.

317. The method of Claim 311, wherein said agent which reduces the activity or level of a gene product required for proliferation of said cell comprises a compound known to inhibit growth or proliferation of a cell.

318. The method of Claim 311, wherein said cell contains a mutation which reduces the activity or level of said gene product required for proliferation of said cell.

319. The method of Claim 311, wherein said mutation is a temperature sensitive mutation.

320. The method of Claim 311, wherein said gene product comprises a gene product comprises a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42398-78581.

321. A compound identified using the method of Claim 311.

322. A method for identifying the biological pathway in which a proliferation-required gene product or a gene encoding a proliferation-required gene product lies comprising:

(a) providing a sublethal level of an antisense nucleic acid which inhibits the activity or reduces the level of said gene encoding a proliferation-required gene product or said said proliferation-required gene product in a test cell, wherein said proliferation-required gene product is selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group

consisting of SEQ ID NOs:1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 1-6213;

(b) contacting said test cell with a compound known to inhibit growth or proliferation of a cell, wherein the biological pathway on which said compound acts is known; and

(c) determining the degree to which said compound inhibits proliferation of said test cell relative to a cell which does not contain said antisense nucleic acid.

323. The method of Claim 322, wherein said determining step comprises determining whether said test cell has a substantially greater sensitivity to said compound than a cell which does not express said sublethal level of said antisense nucleic acid.

324. The method of Claim 322, wherein said gene product comprises a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42398-78581.

325. The method of Claim 322, wherein said test cell is selected from the group consisting of Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis,

Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

326. The method of Claim 322, wherein said test cell is not an *E. coli* cell.

327. The method of Claim 322, wherein said gene product is from an organism other than *E. coli*.

328. A method for determining the biological pathway on which a test compound acts comprising:

(a) providing a sublethal level of an antisense nucleic acid complementary to a proliferation-required nucleic acid in a cell, thereby producing a sensitized cell, wherein said antisense nucleic acid is selected from the group consisting of a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-6213 or a proliferation-inhibiting portion thereof,a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions and wherein the biological pathway in which said proliferation-required nucleic acid or a protein encoded by said proliferation-required polypeptide lies is known,

(b) contacting said cell with said test compound; and

(c) determining the degree to which said compound inhibits proliferation of said sensitized cell relative to a cell which does not contain said antisense nucleic acid.

329. The method of Claim 328, wherein said determining step comprises determining whether said sensitized cell has a substantially greater sensitivity to said test compound than a cell which does not express said sublethal level of said antisense nucleic acid.

330. The method of Claim 328, further comprising:

(d) providing a sublethal level of a second antisense nucleic acid complementary to a second proliferation-required nucleic acid in a second cell, wherein said second proliferation-required nucleic acid is in a different biological pathway than said proliferation-required nucleic acid in step (a); and

(e) determining whether said second cell does not have a substantially greater sensitivity to said test compound than a cell which does not express said sublethal level of said second antisense nucleic acid, wherein said test compound is specific for the biological pathway against which the antisense nucleic acid of step (a) acts if said sensitized cell has substantially greater sensitivity to said test compound than said second cell.

331. The method of Claim 328, wherein said sensitized cell is selected from the group consisting of Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

332. The method of Claim 328, wherein said sensitized cell is not an *E. coli* cell.

333. The method of Claim 328, wherein said proliferation-required nucleic acid is from an organism other than *E. coli*.

334. A compound which inhibits proliferation by interacting with a gene encoding a gene product required for proliferation or with a gene product required for proliferation, wherein said gene product is selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 1-6213.

335. The compound of Claim 334, wherein said gene product comprises a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a sequence selected from the group consisting of SEQ ID NOs.: 42398-78581.

336. The compound of Claim 334, wherein said gene comprises a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate condtions.

337. A method for manufacturing an antibiotic comprising the steps of:

screening one or more candidate compounds to identify a compound that reduces the activity or level of a gene product required for proliferation wherein said gene product is selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 1-6213 ; and

manufacturing the compound so identified.

338. The method of Claim 337, wherein said screening step comprises performing any one of the methods of Claims 205, 211, 222, 275, 290, 295, 311.

339. The method of Claim 337, wherein said gene product comprises a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42398-78581.

340. A method for inhibiting proliferation of a cell in a subject comprising administering an effective amount of a compound that reduces the activity or level of a gene product required for proliferation of said cell, wherein said gene product is selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with

the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 1-6213.

341. The method of Claim 340 wherein said subject is selected from the group consisting of vertebrates, mammals, avians, and human beings.

342. The method of Claim 340, wherein said gene product comprises a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42398-78581.

343. The method of Claim 340, wherein said cell is selected from the group consisting of Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata (also called Torulopsis glabrata), Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr (also called Candida pseudotropicalis), Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi,

Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

344. The method of Claim 340, wherein said cell is not *E. coli*.

345. The method of Claim 340, wherein said gene product is from an organism other than *E. coli*.

346. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain in said culture overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 is overexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture.

347. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain in said culture overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397 is overexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture.

348. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain in said culture overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42938-78581 is overexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture.

349. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain in said culture overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent

conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213 is overexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture.

350. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain in said culture overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate conditions is overexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture.

351. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain in said culture overexpresses a different gène product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 42938-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 42938-78581 is overexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture.

352. The method of Claim 346, 347, 348, 349, 350 or 351, wherein said culture includes at least one strain which does not overexpresses a gene product which is essential for proliferation of said organism.

353. The method of Claim 346, 347, 348, 349, 350 or 351, wherein said strains which overexpress said gene products comprise a nucleic acid encoding said gene product which is essential for proliferation of said organism operably linked to a regulatable promoter.

354. The method of Claim 346, 347, 348, 349, 350 or 351, wherein said strains which overexpress said gene products a nucleic acid encoding said gene product which is essential for proliferation of said organism operably linked to a constitutive promoter.

355. The method of Claim 346, 347, 348, 349, 350 or 351, wherein said identification step comprises determining the nucleotide sequence of a nucleic acid encoding said gene product in said cell which proliferated more rapidly in said culture.

356. The method of Claim 346, 347, 348, 349, 350 or 351, wherein said identification step comprises performing an amplification reaction to identify the nucleic acid encoding said gene product in said cell which proliferated more rapidly in said cell culture.

357. The method of Claim 356, wherein the products of said amplification reaction are labeled with a detectable dye.

358. The method of Claim 346, 347, 348, 349, 350 or 351, wherein said identification step comprises performing a hybridization procedure.

359. The method of Claim 346, 347, 348, 349, 350 or 351, wherein said identification step comprises contacting a nucleic acid array with a nucleic acid encoding said gene product in said cell which proliferated more rapidly in said cell culture.

360. The method of Claim 346, 347, 348, 349, 350 or 351, wherein said organism is selected from the group consisting of bacteria, fungi, and protozoa.

361. The method of Claim 346, 347, 348, 349, 350 or 351, wherein said culture is a culture of an organism selected from the group consisting of *Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

362. The method of Claim 346, 347, 348, 349, 350 or 351, wherein said compound is obtained from a library of natural compounds.

363. The method of Claim 346, 347, 348, 349, 350 or 351, wherein said compound is obtained from a library of synthetic compounds.

364. The method of Claim 346, 347, 348, 349, 350 or 351, wherein said compound is present in a crude or partially purified state.

365. The method of Claim 346, 347, 348, 349, 350 or 351, further comprising determining whether said gene product in said strain which proliferated more rapidly in said culture has a counterpart in at least one other organism.

366. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining an array of strains on a solid growth medium wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 is overexpressed;

contacting said array of strains with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly on said solid medium.

367. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining an array of strains on a solid growth medium wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397 is overexpressed;

contacting said array of strains with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly on said solid medium.

368. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining an array of strains on a solid growth medium wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42938-78581 is overexpressed;

contacting said array of strains with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly on said solid medium.

369. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining an array of strains on a solid growth medium wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide

sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213 is overexpressed;

contacting said array of strains with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly on said solid medium.

370. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining an array of strains on a solid growth medium wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate conditions is overexpressed;

contacting said array of strains with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly on said solid medium.

371. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining an array of strains on a solid growth medium wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 42938-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 42938-78581 is overexpressed;

contacting said array of strains with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly on said solid medium.

372. The method of Claim 366, 367, 368, 369, 370 or 371, wherein at least one strain in said array does not overexpresses a gene product which is essential for proliferation of said organism.

373. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a plurality of cultures, wherein each culture comprises a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 is overexpressed;

contacting each of said cultures with a different concentration of said compound; and

identifying the gene product which is overexpressed in a strain whose proliferation is inhibited by said compound.

374. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a plurality of cultures, wherein each culture comprises a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397 is overexpressed;

contacting each of said cultures with a different concentration of said compound; and

identifying the gene product which is overexpressed in a strain whose proliferation is inhibited by said compound.

375. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a plurality of cultures, wherein each culture comprises a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42938-78581 is overexpressed;

contacting each of said cultures with a different concentration of said compound; and

identifying the gene product which is overexpressed in a strain whose proliferation is inhibited by said compound.

376. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a plurality of cultures, wherein each culture comprises a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product

whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213 is overexpressed;

contacting each of said cultures with a different concentration of said compound; and

identifying the gene product which is overexpressed in a strain whose proliferation is inhibited by said compound.

377. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a plurality of cultures, wherein each culture comprises a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate conditions is overexpressed;

contacting each of said cultures with a different concentration of said compound; and

identifying the gene product which is overexpressed in a strain whose proliferation is inhibited by said compound.

378. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a plurality of cultures, wherein each culture comprises a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 42938-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 42938-78581 is overexpressed;

contacting each of said cultures with a different concentration of said compound; and

identifying the gene product which is overexpressed in a strain whose proliferation is inhibited by said compound.

379. The method of Claim 373, 374, 375, 376, 377 or 378, wherein at least one strain in said plurality of cultures does not overexpress a gene product which is essential for proliferation of said organism.

380. A method of profiling a compound's activity comprising:

performing the method of Claim 346 on a first culture using a first compound;

performing the method of Claim 346 on a second culture using a second compound; and

comparing the strains identified in said first culture to the strains identified in said second culture.

381. A method of profiling a compound's activity comprising:

performing the method of Claim 347 on a first culture using a first compound;

performing the method of Claim 347 on a second culture using a second compound; and

comparing the strains identified in said first culture to the strains identified in said second culture.

382. A method of profiling a compound's activity comprising:

performing the method of Claim 348 on a first culture using a first compound;

performing the method of Claim 348 on a second culture using a second compound; and

comparing the strains identified in said first culture to the strains identified in said second culture.

383. A method of profiling a compound's activity comprising:

performing the method of Claim 349 on a first culture using a first compound;

performing the method of Claim 349 on a second culture using a second compound; and

comparing the strains identified in said first culture to the strains identified in said second culture.

384. A method of profiling a compound's activity comprising:

performing the method of Claim 350 on a first culture using a first compound;

performing the method of Claim 350 on a second culture using a second compound; and

comparing the strains identified in said first culture to the strains identified in said second culture.

385. A method of profiling a compound's activity comprising:

performing the method of Claim 351 on a first culture using a first compound;

performing the method of Claim 351 on a second culture using a second compound; and

comparing the strains identified in said first culture to the strains identified in said second culture.

386. A method of profiling a first compound's activity comprising:

growing an array of strains on a first solid medium comprising said first compound and on a second solid medium comprising a second compound, wherein each strain in said array overexpresses a different gene product which is essential for proliferation of an organism, wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 is overexpressed, and wherein said first compound and said second compound inhibit the proliferation of said organism; and

comparing the pattern of strains which grow on said first solid medium with the pattern of strains which grow on said second solid medium.

387. A method of profiling a first compound's activity comprising:

growing an array of strains on a first solid medium comprising said first compound and on a second solid medium comprising a second compound, wherein each strain in said array overexpresses a different gene product which is essential for proliferation of an organism, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397 is overexpressed, and wherein said first compound and said second compound inhibit the proliferation of said organism; and

comparing the pattern of strains which grow on said first solid medium with the pattern of strains which grow on said second solid medium.

388. A method of profiling a first compound's activity comprising:

growing an array of strains on a first solid medium comprising said first compound and on a second solid medium comprising a second compound, wherein each strain in said array overexpresses a different gene product which is essential for proliferation of an organism, wherein said culture comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42938-78581 is overexpressed, and wherein said first compound and said second compound inhibit the proliferation of said organism; and

comparing the pattern of strains which grow on said first solid medium with the pattern of strains which grow on said second solid medium.

389. A method of profiling a first compound's activity comprising:

growing an array of strains on a first solid medium comprising said first compound and on a second solid medium comprising a second compound, wherein each strain in said array overexpresses a different gene product which is essential for proliferation of an organism, wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid

comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213 is overexpressed, and wherein said first compound and said second compound inhibit the proliferation of said organism; and

comparing the pattern of strains which grow on said first solid medium with the pattern of strains which grow on said second solid medium.

390. A method of profiling a first compound's activity comprising:

growing an array of strains on a first solid medium comprising said first compound and on a second solid medium comprising a second compound, wherein each strain in said array overexpresses a different gene product which is essential for proliferation of an organism, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate conditions is overexpressed, and wherein said first compound and said second compound inhibit the proliferation of said organism; and

comparing the pattern of strains which grow on said first solid medium with the pattern of strains which grow on said second solid medium.

391. A method of profiling a first compound's activity comprising:

growing an array of strains on a first solid medium comprising said first compound and on a second solid medium comprising a second compound, wherein each strain in said array overexpresses a different gene product which is essential for proliferation of an organism, wherein said culture comprises a strain in which a gene product comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 42938-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 42938-78581 is overexpressed, and wherein said first compound and said second compound inhibit the proliferation of said organism; and

comparing the pattern of strains which grow on said first solid medium with the pattern of strains which grow on said second solid medium.

392. The method of any one of Claims 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390 or 391, wherein said first compound is present in a crude or partially purified state.

393. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 is underexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress said gene product on which said compound acts; and

identifying the gene product which is underexpressed in a strain which proliferated more slowly in said culture.

394. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397 is underexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress said gene product on which said compound acts; and

identifying the gene product which is underexpressed in a strain which proliferated more slowly in said culture.

395. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product comprising

an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42938-78581 is underexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress said gene product on which said compound acts; and

identifying the gene product which is underexpressed in a strain which proliferated more slowly in said culture.

396. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213 is underexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene

product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress said gene product on which said compound acts; and

identifying the gene product which is underexpressed in a strain which proliferated more slowly in said culture.

397. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate conditions is underexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress said gene product on which said compound acts; and

identifying the gene product which is underexpressed in a strain which proliferated more slowly in said culture.

398. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 42938-78581 and a polypeptide

whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 42938-78581 is underexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress said gene product on which said compound acts; and

identifying the gene product which is underexpressed in a strain which proliferated more slowly in said culture.

399. The method of Claim 393, 394, 395, 396, 397 or 398, wherein at least one strain in said culture does not underexpresses a gene product which is essential for proliferation of said organism.

400. The method of Claim 393, 394, 395, 396, 397 or 398, wherein said strains which underexpresess said gene products comprise a nucleic acid complementary to at least a portion of a gene encoding said gene product which is essential for proliferation of said organism operably linked to a regulatable promoter.

401. The method of Claim 393, 394, 395, 396, 397 or 398, wherein said strains which underexpress said gene products express an antisense nucleic acid complementary to at least a portion of a gene encoding said gene product which is essential for proliferation of said organism, wherein expression of said antisense nucleic acid reduces expression of said gene product in said strain.

402. The method of Claim 393, 394, 395, 396, 397 or 398, wherein said identification step comprises determining the nucleotide sequence of a nucleic acid encoding said gene product in said strain which proliferated more slowly.

403. The method of Claim 393, 394, 395, 396, 397 or 398, wherein said identification step comprises performing an amplification reaction to identify the nucleic acid encoding said gene product in said cell which proliferated more slowly.

404. The method of Claim 393, 394, 395, 396, 397 or 398, wherein the products of said amplification reaction are labeled with a detectable dye.

405. The method of Claim 404, wherein said identification step comprises performing a hybridization procedure.

406. The method of Claim 393, 394, 395, 396, 397 or 398, wherein said identification step comprises contacting a nucleic acid array with a nucleic acid encoding said gene product in said cell which proliferated more slowly.

407. The method of Claim 393, 394, 395, 396, 397 or 398, wherein said organism is selected from the group consisting of bacteria, fungi, protozoa.

408. The method of Claim 393, 394, 395, 396, 397 or 398, wherein said culture is a culture of an organism selected from the group consisting of *Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

409. The method of Claim 393, 394, 395, 396, 397 or 398, wherein said compound is obtained from a library of natural compounds.

410. The method of Claim 393, 394, 395, 396, 397 or 398, wherein said compound is obtained from a library of synthetic compounds.

411. The method of Claim 393, 394, 395, 396, 397 or 398, wherein said compound is present in a crude or partially purified state.

412. The method of Claim 393, 394, 395, 396, 397 or 398, further comprising determining whether said gene product in said strain which proliferated more slowly in said culture has a counterpart in at least one other organism.

413. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a plurality of cultures, each culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 is underexpressed;

contacting each of said cultures with a different concentration of said compound; and

identifying the gene product which is underexpressed in a strain whose rate of proliferation is reduced by said compound.

414. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a plurality of cultures, each culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397 is underexpressed;

contacting each of said cultures with a different concentration of said compound; and

identifying the gene product which is underexpressed in a strain whose rate of proliferation is reduced by said compound.

415. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a plurality of cultures, each culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42938-78581 is underexpressed;

contacting each of said cultures with a different concentration of said compound; and

identifying the gene product which is underexpressed in a strain whose rate of proliferation is reduced by said compound.

416. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a plurality of cultures, each culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213 is underexpressed;

contacting each of said cultures with a different concentration of said compound; and

identifying the gene product which is underexpressed in a strain whose rate of proliferation is reduced by said compound.

417. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a plurality of cultures, each culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the

group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate conditions is underexpressed;

contacting each of said cultures with a different concentration of said compound; and

identifying the gene product which is underexpressed in a strain whose rate of proliferation is reduced by said compound.

418. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a plurality of cultures, each culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 42938-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 42938-78581 is underexpressed;

contacting each of said cultures with a different concentration of said compound; and

identifying the gene product which is underexpressed in a strain whose rate of proliferation is reduced by said compound.

419. A method of profiling a compound's activity comprising:

performing the method of Claim 393 on a first culture using a first compound;

performing the method of Claim 393 on a second culture using a second compound; and

comparing the strains identified in said first culture to the strains identified in said second culture.

420. A method of profiling a compound's activity comprising:

performing the method of Claim 394 on a first culture using a first compound;

performing the method of Claim 394 on a second culture using a second compound; and

comparing the strains identified in said first culture to the strains identified in said second culture.

421. A method of profiling a compound's activity comprising:

performing the method of Claim 395 on a first culture using a first compound;

performing the method of Claim 395 on a second culture using a second compound; and

comparing the strains identified in said first culture to the strains identified in said second culture.

422. A method of profiling a compound's activity comprising

performing the method of Claim 396 on a first culture using a first compound;

performing the method of Claim 396 on a second culture using a second compound; and

comparing the strains identified in said first culture to the strains identified in said second culture.

423. A method of profiling a compound's activity comprising

performing the method of Claim 397 on a first culture using a first compound;

performing the method of Claim 397 on a second culture using a second compound; and

comparing the strains identified in said first culture to the strains identified in said second culture.

424. A method of profiling a compound's activity comprising

performing the method of Claim 398 on a first culture using a first compound;

performing the method of Claim 398 on a second culture using a second compound; and

comparing the strains identified in said first culture to the strains identified in said second culture.

425. A method of profiling a first compound's activity comprising:

growing an array of strains on a first solid medium comprising said first compound and on a second solid medium comprising a second compound, wherein said array comprises a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of an organism, wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of

SEQ ID NOs.: 1-6213 is underexpressed, and wherein said first compound and said second compound inhibit the proliferation of said organism; and

comparing the pattern of strains which grow on said first solid medium with the pattern of strains which grow on said second solid medium.

426. A method of profiling a first compound's activity comprising:

growing an array of strains on a first solid medium comprising said first compound and on a second solid medium comprising a second compound, wherein said array comprises a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of an organism, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397 is underexpressed, and wherein said first compound and said second compound inhibit the proliferation of said organism; and

comparing the pattern of strains which grow on said first solid medium with the pattern of strains which grow on said second solid medium.

427. A method of profiling a first compound's activity comprising:

growing an array of strains on a first solid medium comprising said first compound and on a second solid medium comprising a second compound, wherein said array comprises a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of an organism, wherein said culture comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42938-78581 is underexpressed, and wherein said first compound and said second compound inhibit the proliferation of said organism; and

comparing the pattern of strains which grow on said first solid medium with the pattern of strains which grow on said second solid medium.

428. A method of profiling a first compound's activity comprising:

growing an array of strains on a first solid medium comprising said first compound and on a second solid medium comprising a second compound, wherein said array comprises a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of an organism, wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group

consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213 is underexpressed, and wherein said first compound and said second compound inhibit the proliferation of said organism; and

comparing the pattern of strains which grow on said first solid medium with the pattern of strains which grow on said second solid medium.

429. A method of profiling a first compound's activity comprising:

growing an array of strains on a first solid medium comprising said first compound and on a second solid medium comprising a second compound, wherein said array comprises a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of an organism , wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate conditions is underexpressed, and wherein said first compound and said second compound inhibit the proliferation of said organism; and

comparing the pattern of strains which grow on said first solid medium with the pattern of strains which grow on said second solid medium.

430. A method of profiling a first compound's activity comprising:

growing an array of strains on a first solid medium comprising said first compound and on a second solid medium comprising a second compound, wherein said array comprises a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of an organism, wherein said culture comprises a strain in which a gene product comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 42938-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 42938-78581 is underexpressed, and wherein said first compound and said second compound inhibit the proliferation of said organism; and

comparing the pattern of strains which grow on said first solid medium with the pattern of strains which grow on said second solid medium.

431. The method of any one of Claims 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429 or 430, wherein said first compound is present in a crude or partially purified state.

432. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a plurality of cultures comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 is underexpressed;

contacting each of said plurality of cultures with a varying concentration of a regulatory agent which regulates the level of expression of said gene products which are essential for proliferation of said organism; and

identifying the gene product which is underexpressed in a strain whose rate of proliferation is reduced by said compound.

433. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a plurality of cultures comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product encoded by a

nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397 is underexpressed;

contacting each of said plurality of cultures with a varying concentration of a regulatory agent which regulates the level of expression of said gene products which are essential for proliferation of said organism; and

identifying the gene product which is underexpressed in a strain whose rate of proliferation is reduced by said compound.

434. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a plurality of cultures comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42938-78581 is underexpressed;

contacting each of said plurality of cultures with a varying concentration of a regulatory agent which regulates the level of expression of said gene products which are essential for proliferation of said organism; and

identifying the gene product which is underexpressed in a strain whose rate of proliferation is reduced by said compound.

435. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a plurality of cultures comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from

the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213 is underexpressed;

contacting each of said plurality of cultures with a varying concentration of a regulatory agent which regulates the level of expression of said gene products which are essential for proliferation of said organism; and

identifying the gene product which is underexpressed in a strain whose rate of proliferation is reduced by said compound.

436. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a plurality of cultures comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate conditions is underexpressed;

contacting each of said plurality of cultures with a varying concentration of a regulatory agent which regulates the level of expression of said gene products which are essential for proliferation of said organism; and

identifying the gene product which is underexpressed in a strain whose rate of proliferation is reduced by said compound.

437. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a plurality of cultures comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 42938-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 42938-78581 is underexpressed;

contacting each of said plurality of cultures with a varying concentration of a regulatory agent which regulates the level of expression of said gene products which are essential for proliferation of said organism; and

identifying the gene product which is underexpressed in a strain whose rate of proliferation is reduced by said compound.

438. A culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 is overexpressed.

439. A culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397 is overexpressed.

440. A culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42938-78581 is overexpressed.

441. A culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising

a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213 is overexpressed.

442. A culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate conditions is overexpressed.

443. A culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 42938-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 42938-78581 is overexpressed.

444. The culture of Claim 438, 439, 440, 441, 442 or 443, wherein said strains which overexpresess said gene products comprise a nucleic acid encoding said gene product which is essential for proliferation of said organism operably linked to a regulatable promoter.

445. The culture of Claim 438, 439, 440, 441, 442 or 443, wherein said strains which overexpresess said gene products comprise a nucleic acid encoding said gene product which is essential for proliferation of said organism operably linked to a constitutive promoter.

446. The culture of Claim 438, 439, 440, 441, 442 or 443, wherein said culture is a culture of an organism selected from the group consisting of *Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

447. A culture comprising a a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 is underexpressed.

448. A culture comprising a a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a

nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397 is underexpressed.

449. A culture comprising a a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42938-78581 is underexpressed.

450. A culture comprising a a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213 is underexpressed.

451. A culture comprising a a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent

conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate conditions is underexpressed.

452. A culture comprising a a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 42938-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 42938-78581 is underexpressed.

453. The culture of Claim 447, 448, 449, 450, 451 or 452, wherein said strains which underexpress said gene products comprise a nucleic acid encoding said gene product which is essential for proliferation of said organism operably linked to a regulatable promoter.

454. The culture of Claim 447, 448, 449, 450, 451 or 452, wherein said strains which underexpress said gene products comprise a nucleic acid encoding said gene product which is essential for proliferation of said organism operably linked to a constitutive promoter.

455. The culture of Claim 447, 448, 449, 450, 451 or 452, wherein said culture is a culture of an organism selected from the group consisting of *Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella*

sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

456. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the overexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the overexpressed genes, wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 is overexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

457. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the overexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the overexpressed genes, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397 is overexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene

product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

458. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the overexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the overexpressed genes, wherein said culture comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42938-78581 is overexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

459. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the overexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the overexpressed genes, wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at

least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213 is overexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

460. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the overexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the overexpressed genes, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a

nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate conditions is overexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

461. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the overexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the overexpressed genes, wherein said culture comprises a strain in which a gene product comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 42938-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 42938-78581 is overexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

462. The method of Claim 456, 457, 458, 459, 460 or 461, wherein the nucleotide sequence of each of the genes encoding an overexpressed gene product has been altered by replacing the native promoters of said genes with promoters which facilitate overexpression of said gene products.

463. The method of Claim 456, 457, 458, 459, 460 or 461, wherein the nucleotide sequence of each of the genes encoding an overexpressed gene product has been altered by inserting a regulatory element into the native promoters of said genes with a promoter which facilitates overexpression of said gene products.

464. The method of Claim 463, wherein said regulatory element is selected from the group consisting of a regulatable promoter, an operator which is recognized by a repressor, a nucleotide sequence which is recognized by a transcriptional activator, a transcriptional terminator, a nucleotide sequence which introduces a bend in the DNA and an upstream activating sequence.

465. The method of Claim 456, 457, 458, 459, 460 or 461, wherein the step of identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene comprises performing an amplification reaction and detecting a unique amplification product corresponding to said gene.

466. The method of Claim 462, wherein the native promoter of each of the genes encoding a gene product essential for proliferation is replaced with the same promoter.

467. The method of Claim 462, wherein the native promoters of the genes encoding gene products essential for proliferation are replaced with a plurality of promoters selected to give a desired expression level for each gene product.

468. The method of Claim 462, wherein said promoters which replaced the native promoters in each strain comprise regulatable promoters.

469. The method of Claim 462, wherein said promoters which replaced the native promoters in each strain each strain comprise constitutive promoters.

470. The method of Claim 456, 457, 458, 459, 460 or 461, wherein said organism is selected from the group consisting of bacteria, fungi, and protozoa.

471. The method of Claim 456, 457, 458, 459, 460 or 461, wherein said culture is a culture of an organism selected from the group consisting of *Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis, Candida parapsilosis, Candida guilliermondii,*

Candida krusei, Candida kefyr (also called *Candida pseudotropicalis*), *Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

472. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the underexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the underexpressed genes and wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 is underexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress the gene product on which said compound acts; and

identifying the gene product which is underexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

473. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the underexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the underexpressed genes and wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397 is underexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress the gene product on which said compound acts; and

identifying the gene product which is underexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

474. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the underexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the underexpressed genes, wherein said culture comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42938-78581 is underexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress the gene product on which said compound acts; and

identifying the gene product which is underexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

475. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the underexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the underexpressed genes, wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213 is underexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress the gene product on which said compound acts; and

identifying the gene product which is underexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

476. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the underexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the underexpressed genes, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate conditions is underexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress the gene product on which said compound acts; and

identifying the gene product which is underexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

477. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the underexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the underexpressed genes , wherein said

culture comprises a strain in which a gene product comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 42938-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 42938-78581 is underexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress the gene product on which said compound acts; and

identifying the gene product which is underexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

478. The method of Claim 472, 473, 474, 475, 476 or 477, wherein the nucleotide sequence of each of the genes encoding an underexpressed gene product has been altered by replacing the native promoters of said genes with promoters which facilitate underexpression of said gene products.

479. The method of Claim 472, 473, 474, 475, 476 or 477, wherein the nucleotide sequence of each of the genes encoding an underexpressed gene product has been altered by inserting a regulatory element into the native promoters of said genes with a promoter which facilitates underexpression of said gene products.

480. The method of Claim 479, wherein said regulatory element is selected from the group consisting of a regulatable promoter, an operator which is recognized by a repressor, a nucleotide sequence which is recognized by a transcriptional activator, a transcriptional terminator, a nucleotide sequence which introduces a bend in the DNA and an upstream activating sequence.

481. The method of Claim 472, 473, 474, 475, 476 or 477, wherein the step of identifying the gene product which is underexpressed in a strain which proliferated more slowly in said culture by detecting the unique product corresponding to said gene comprises performing an amplification reaction and detecting a unique amplification product corresponding to said gene.

482. The method of Claim 478, wherein the native promoter of each of the genes encoding a gene product essential for proliferation is replaced with the same promoter.

483. The method of Claim 478, wherein the native promoters of the genes encoding gene products essential for proliferation are replaced with a plurality of promoters selected to give a desired expression level for each gene product.

484. The method of Claim 478, wherein said promoters which replaced the native promoters in each strain comprise regulatable promoters.

485. The method of Claim 478, wherein said promoters which replaced the native promoters in each strain each strain comprise constitutive promoters.

486. The method of Claim 472, 473, 474, 475, 476 or 477, wherein said organism is selected from the group consisting of bacteria, fungi, and protozoa.

487. The method of Claim 472, 473, 474, 475, 476 or 477, wherein said culture is a culture of an organism selected from the group consisting of *Acinetobacter baumannii, Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacteroides fragilis, Bordetella pertussis, Borrelia burgdorferi, Burkholderia cepacia, Burkholderia fungorum, Burkholderia mallei, Campylobacter jejuni, Candida albicans, Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatis, Clostridium acetobutylicum, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidioides immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Legionella pneumophila, Listeria monocytogenes, Moraxella catarrhalis, Mycobacterium avium, Mycobacterium bovis, Mycobacterium leprae, Mycobacterium tuberculosis, Mycoplasma genitalium, Mycoplasma pneumoniae, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus mirabilis, Proteus vulgaris, Pseudomonas aeruginosa, Pseudomonas putida, Pseudomonas syringae, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus haemolyticus, Streptococcus pneumoniae, Streptococcus mutans, Streptococcus pyogenes, Treponema pallidum, Ureaplasma urealyticum, Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificans, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

488. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 is overexpressed or underexpressed;

performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction.

489. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism , wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397 is overexpressed or underexpressed;

performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction.

490. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism, wherein said culture comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42938-78581 is overexpressed or underexpressed;

performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction.

491. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism , wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a

gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213 is overexpressed or underexpressed;

performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction.

492. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism , wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate conditions is overexpressed or underexpressed;

performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode

said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction.

493. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism , wherein said culture comprises a strain in which a gene product comprising a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 42938-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 42938-78581 is overexpressed or underexpressed;

performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction.

494. The method of Claim 488, 489, 490, 491, 492 or 493, wherein one member of each primer pair for each of said genes is labeled with a detectable dye.

495. The method of Claim 488, 489, 490, 491, 492 or 493, wherein:

said nucleic acid sample is divided into N aliquots; and

said amplification reaction is performed on each aliquot using primer pairs complementary to nucleotide sequences within or adjacent to 1/N of the genes which encode said gene products, wherein one of the members of each primer pair in each

aliquot is labeled with a dye and wherein the dyes on the primers in each aliquot are distinguishable from one another.

496. The method of Claim 494, further comprising pooling the amplification products from each of the aliquots prior to determining the lengths of the amplification products.

497. The method of Claim 488, 489, 490, 491, 492 or 493, wherein the native promoters of said genes which encode said gene products have been replaced with a regulatable promoter and one of the primers in said primer pairs is complementary to a nucleotide sequence within said regulatable promoter.

498. The method of Claim 496, wherein the native promoters for each of said genes were replaced with the same regulatable promoter.

499. The method of Claim 496, wherein more than one regulatable promoter was used to replace the promoters of said genes such that some of said genes are under the control of a different regulatable promoter.

500. A method for identifying the target of a compound which inhibits the proliferation of an organism comprising:

obtaining a first nucleic acid sample comprising nucleic acids from a first culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism and wherein said culture or collection of strains has been contacted with said compound;

obtaining a second nucleic acid sample comprising nucleic acids from a second culture or collection of strains wherein said culture or collection of strains comprises the same strains as said first culture or collection of strains wherein said second culture or collection of strains has not been contacted with said compound;

performing a first amplification reaction on said first nucleic acid sample using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains;

performing a second amplification reaction on said second nucleic acid sample using the same set of primer pairs used in said first amplification reaction;

and comparing the amount of each amplification product in said first amplification reaction to the amount of that amplification product in said second amplification reaction, wherein an increased level of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products and a decreased level of of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products, wherein said first and second cultures or collection of strains comprise a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 is overexpressed or underexpressed.

501. A method for identifying the target of a compound which inhibits the proliferation of an organism comprising:

obtaining a first nucleic acid sample comprising nucleic acids from a first culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism and wherein said culture or collection of strains has been contacted with said compound;

obtaining a second nucleic acid sample comprising nucleic acids from a second culture or collection of strains wherein said culture or collection of strains comprises the same strains as said first culture or collection of strains wherein said second culture or collection of strains has not been contacted with said compound;

performing a first amplification reaction on said first nucleic acid sample using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains;

performing a second amplification reaction on said second nucleic acid sample using the same set of primer pairs used in said first amplification reaction;

and comparing the amount of each amplification product in said first amplification reaction to the amount of that amplification product in said second

amplification reaction, wherein an increased level of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products and a decreased level of of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products, wherein said first and second cultures or collection of strains comprise a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397 is overexpressed or underexpressed.

502. A method for identifying the target of a compound which inhibits the proliferation of an organism comprising:

obtaining a first nucleic acid sample comprising nucleic acids from a first culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism and wherein said culture or collection of strains has been contacted with said compound;

obtaining a second nucleic acid sample comprising nucleic acids from a second culture or collection of strains wherein said culture or collection of strains comprises the same strains as said first culture or collection of strains wherein said second culture or collection of strains has not been contacted with said compound;

performing a first amplification reaction on said first nucleic acid sample using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains;

performing a second amplification reaction on said second nucleic acid sample using the same set of primer pairs used in said first amplification reaction;

and comparing the amount of each amplification product in said first amplification reaction to the amount of that amplification product in said second amplification reaction, wherein an increased level of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that

the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products and a decreased level of of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products, wherein said first and second cultures or collection of strains comprise a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42938-78581 is overexpressed or underexpressed.

503. A method for identifying the target of a compound which inhibits the proliferation of an organism comprising:

obtaining a first nucleic acid sample comprising nucleic acids from a first culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism and wherein said culture or collection of strains has been contacted with said compound;

obtaining a second nucleic acid sample comprising nucleic acids from a second culture or collection of strains wherein said culture or collection of strains comprises the same strains as said first culture or collection of strains wherein said second culture or collection of strains has not been contacted with said compound;

performing a first amplification reaction on said first nucleic acid sample using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains;

performing a second amplification reaction on said second nucleic acid sample using the same set of primer pairs used in said first amplification reaction;

and comparing the amount of each amplification product in said first amplification reaction to the amount of that amplification product in said second amplification reaction, wherein an increased level of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products and a decreased

level of of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products, wherein said first and second cultures or collection of strains comprise a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213 is overexpressed or underexpressed.

504. A method for identifying the target of a compound which inhibits the proliferation of an organism comprising:

obtaining a first nucleic acid sample comprising nucleic acids from a first culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism and wherein said culture or collection of strains has been contacted with said compound;

obtaining a second nucleic acid sample comprising nucleic acids from a second culture or collection of strains wherein said culture or collection of strains comprises the same strains as said first culture or collection of strains wherein said second culture or collection of strains has not been contacted with said compound;

performing a first amplification reaction on said first nucleic acid sample using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains;

performing a second amplification reaction on said second nucleic acid sample using the same set of primer pairs used in said first amplification reaction;

and comparing the amount of each amplification product in said first amplification reaction to the amount of that amplification product in said second amplification reaction, wherein an increased level of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products and a decreased level of of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products, wherein said first and second cultures or collection of strains comprise a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate conditions is overexpressed or underexpressed.

505. A method for identifying the target of a compound which inhibits the proliferation of an organism comprising:

obtaining a first nucleic acid sample comprising nucleic acids from a first culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene

product which is required for proliferation of said organism and wherein said culture or collection of strains has been contacted with said compound;

obtaining a second nucleic acid sample comprising nucleic acids from a second culture or collection of strains wherein said culture or collection of strains comprises the same strains as said first culture or collection of strains wherein said second culture or collection of strains has not been contacted with said compound;

performing a first amplification reaction on said first nucleic acid sample using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains;

performing a second amplification reaction on said second nucleic acid sample using the same set of primer pairs used in said first amplification reaction;

and comparing the amount of each amplification product in said first amplification reaction to the amount of that amplification product in said second amplification reaction, wherein an increased level of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products and a decreased level of of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products, wherein said first and second culture or collection of strains comprise a strain in which a gene product comprising a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 42938-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 42938-78581 is overexpressed or underexpressed.

506. The method of Claim 500, 501, 502, 503, 504 or 505, wherein one member of each primer pair for each of said genes is labeled with a detectable dye.

507. The method of Claim 500, 501, 502, 503, 504 or 505, wherein the native promoters of said genes which encode said gene products have been replaced with a regulatable

promoter and one of the primers in said primer pairs is complementary to a nucleotide sequence within said regulatable promoter.

508. The method of Claim 500, 501, 502, 503, 504 or 505, wherein the native promoters for each of said genes were replaced with the same regulatable promoter.

509. The method of Claim 500, 501, 502, 503, 504 or 505, wherein more than one regulatable promoter was used to replace the promoters of said genes such that some of said genes are under the control of a different regulatable promoter.

510. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which transcribe an antisense nucleic acid complementary to a different gene product which is required for proliferation of said organism;

performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the nucleic acids which encode said antisense nucleic acids, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 is overexpressed or underexpressed.

511. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which transcribe an antisense nucleic acid complementary to a different gene product which is required for proliferation of said organism;

performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the nucleic acids which encode said antisense nucleic acids, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a

length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397 is overexpressed or underexpressed.

512. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which transcribe an antisense nucleic acid complementary to a different gene product which is required for proliferation of said organism;

performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the nucleic acids which encode said antisense nucleic acids, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42938-78581 is overexpressed or underexpressed.

513. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which transcribe an antisense nucleic acid complementary to a different gene product which is required for proliferation of said organism;

performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the nucleic acids which encode said antisense nucleic acids, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other

primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213 is overexpressed or underexpressed.

514. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which transcribe an antisense nucleic acid complementary to a different gene product which is required for proliferation of said organism;

performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the nucleic acids which encode said antisense nucleic acids, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other

primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate conditions is overexpressed or underexpressed.

515. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which transcribe an antisense nucleic acid complementary to a different gene product which is required for proliferation of said organism;

performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the nucleic acids which encode said antisense nucleic acids, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product comprising a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 42938-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 42938-78581 is overexpressed or underexpressed.

516. The method of Claim 510, 511, 512, 513, 514 or 515, wherein one member of each primer pair for each of said genes is labeled with a detectable dye.

517. The method of Claim 510, 511, 512, 513, 514 or 515, wherein:

said nucleic acid sample is divided into N aliquots; and

said amplification reaction is performed on each aliquot using primer pairs complementary to nucleotide sequences within or adjacent to 1/N of the genes which encode said gene products, wherein one of the members of each primer pair in each aliquot is labeled with a dye and wherein the dyes on the primers in each aliquot are distinguishable from one another.

518. The method of Claim 517, further comprising pooling the amplification products from each of the aliquots prior to determining the lengths of the amplification products.

519. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which overexpress or underexpress a different gene product which is required for proliferation of said organism;

performing an amplification reaction using primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein said primer pairs are designed such that each primer pair would yield an amplification product which is distinguishable from the amplification products produced by the other primer pairs on the a basis selected from the group consisting of length, detectable label and both length and detectable label if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

identifying the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 is overexpressed or underexpressed.

520. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which overexpress or underexpress a different gene product which is required for proliferation of said organism;

performing an amplification reaction using primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein said primer pairs are designed such that each primer pair would yield an amplification product which is distinguishable from the amplification products produced by the other primer pairs on the a basis selected from the group consisting of length, detectable label and both length and detectable label if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

identifying the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397 is overexpressed or underexpressed.

521. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which overexpress or underexpress a different gene product which is required for proliferation of said organism;

performing an amplification reaction using primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein said primer pairs are designed such that each primer pair would yield an amplification product which is distinguishable from the amplification products produced by the other primer pairs on the a basis selected from the group consisting of length, detectable label and both length and detectable label if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

identifying the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42938-78581 is overexpressed or underexpressed.

522. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of

strains which overexpress or underexpress a different gene product which is required for proliferation of said organism;

performing an amplification reaction using primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein said primer pairs are designed such that each primer pair would yield an amplification product which is distinguishable from the amplification products produced by the other primer pairs on the a basis selected from the group consisting of length, detectable label and both length and detectable label if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

identifying the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213 is overexpressed or underexpressed.

523. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which overexpress or underexpress a different gene product which is required for proliferation of said organism;

performing an amplification reaction using primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein said primer pairs are designed such that each primer pair would yield an amplification product which is distinguishable from the amplification products produced by the other primer pairs on the a basis selected from the group consisting of length, detectable label and both length and detectable label if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

identifying the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate conditions is overexpressed or underexpressed.

524. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which overexpress or underexpress a different gene product which is required for proliferation of said organism;

performing an amplification reaction using primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein said primer pairs are designed such that each primer pair would yield an amplification product which is distinguishable from the amplification products produced by the other primer pairs on the a basis selected from the group consisting of length, detectable label and both length and detectable label if a strain

comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

identifying the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product comprising a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 42938-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 42938-78581 is overexpressed or underexpressed.

525. The method of Claim 519, 520, 521, 522, 523 or 524, wherein said primer pairs are divided into at least two sets, each primer pair comprises a primer which is labeled with a distinguishable dye, and the distinguishable dye used to label each set of primer pairs is distinguishable from the dye used to label the other sets of primer pairs.

526. The method of Claim 519, 520, 521, 522, 523 or 524, wherein:

said nucleic acid sample is divided into N aliquots; and

said amplification reaction is performed on each aliquot using primer pairs complementary to nucleotide sequences within or adjacent to 1/N of the genes which encode said gene products, wherein one of the members of each primer pair in each aliquot is labeled with a dye and wherein the dyes on the primers in each aliquot are distinguishable from one another.

527. The method of Claim 526, further comprising pooling the amplification products from each of the aliquots prior to determining the lengths of the amplification products.

528. The method of Claim 519, 520, 521, 522, 523 or 524, wherein the native promoters of said genes which encode said gene products have been replaced with a regulatable promoter and one of the primers in said primer pairs is complementary to a nucleotide sequence within said regulatable promoter.

529. The method of Claim 528, wherein the native promoters for each of said genes were replaced with the same regulatable promoter.

530. The method of Claim 528, wherein more than one regulatable promoter was used to replace the promoters of said genes such that some of said genes are under the control of a different regulatable promoter.

P_R = Regulatable promoter

= Homology region

P_C = Chromosomal promoter

P_S = Promoter operably linked to gene

G_S = Gene encoding selectable or identifiable marker

T_T = Transcriptional terminator

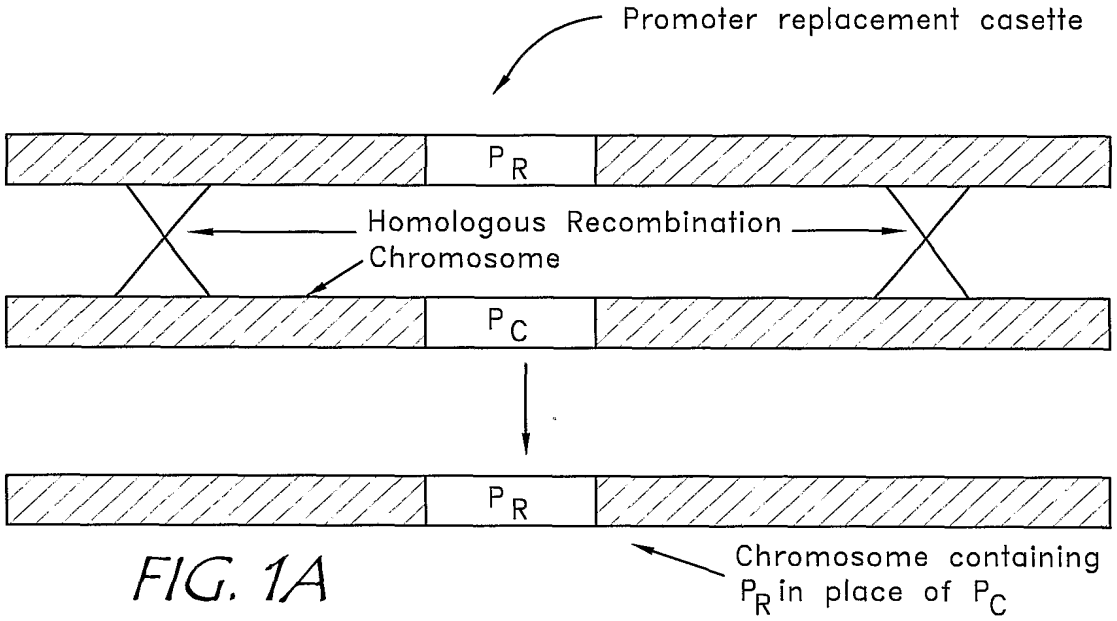


FIG. 1A

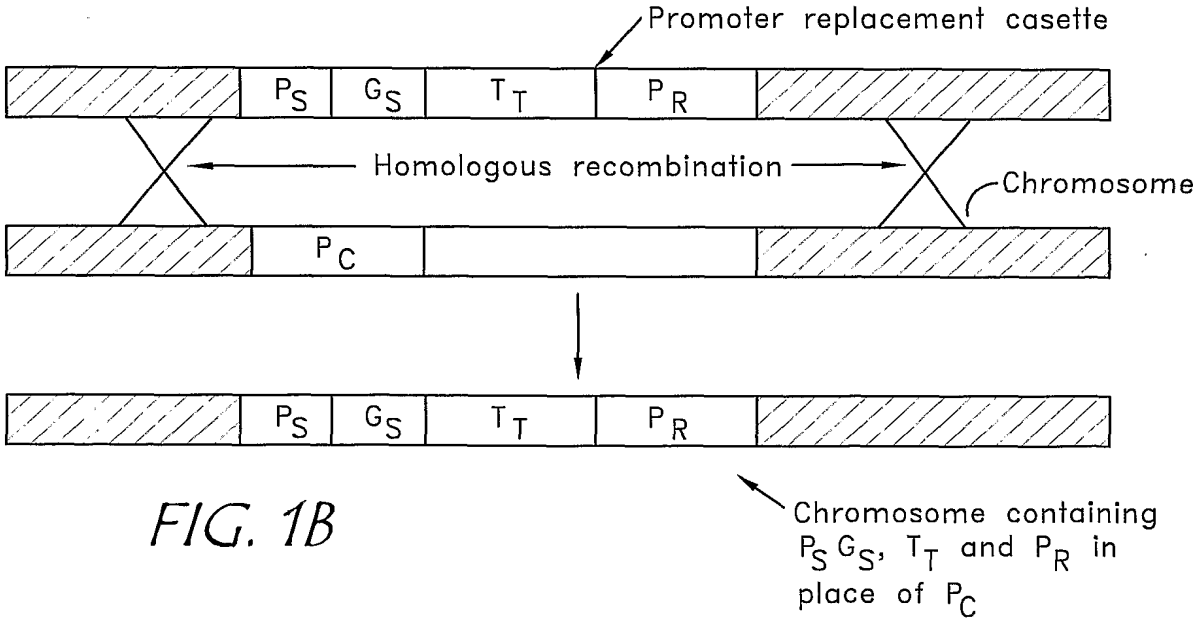


FIG. 1B

FIG. 2

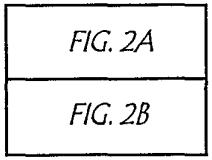


FIG. 2A

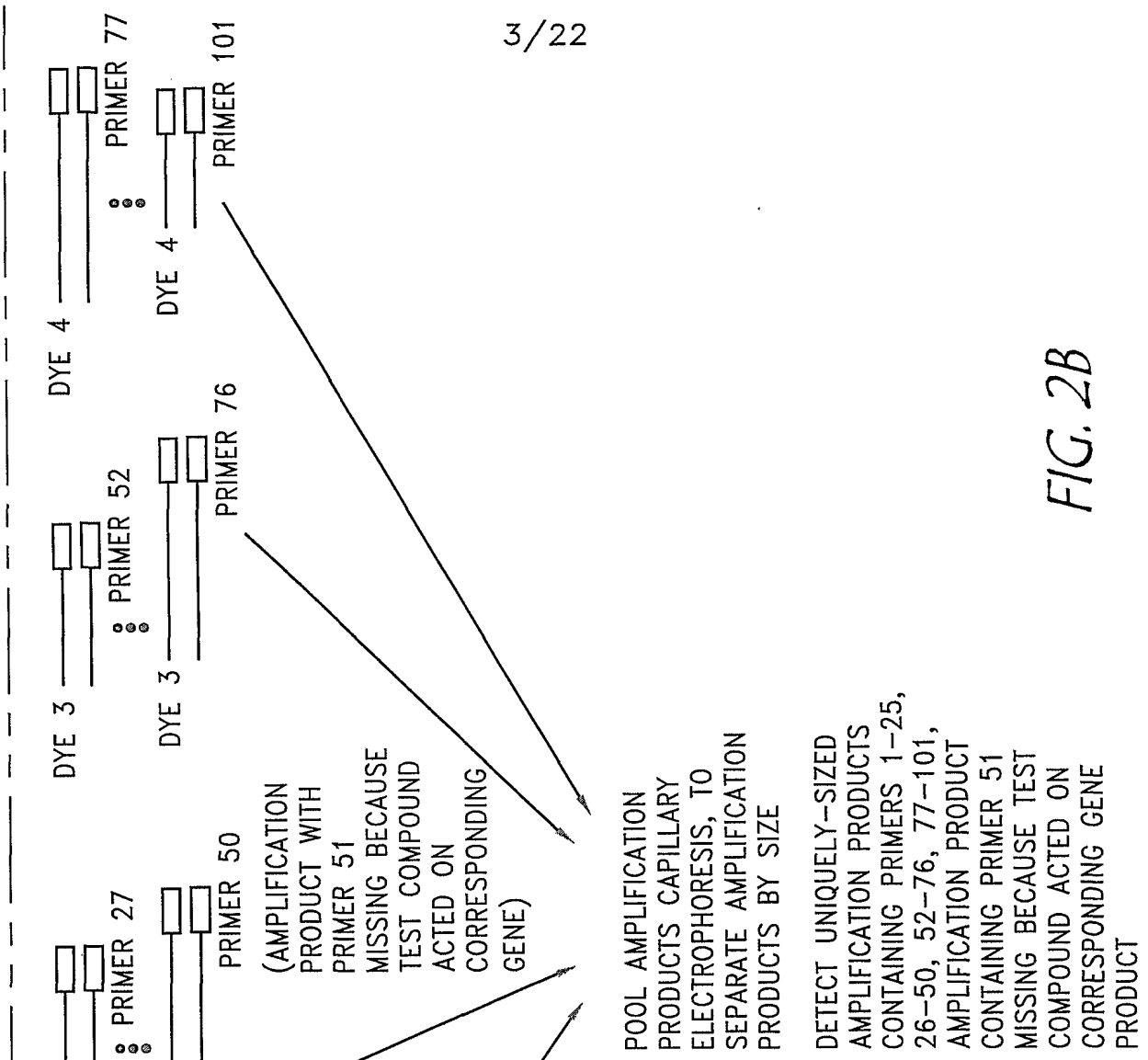

DYE 1
PRIMER 2
PRIMER 26
DYE 2
PRIMER 27
PRIMER 50
DYE 3
PRIMER 52
PRIMER 76
DYE 4
PRIMER 77
PRIMER 101
(AMPLIFICATION PRODUCT WITH PRIMER 51 MISSING BECAUSE TEST COMPOUND ACTED ON CORRESPONDING GENE)
POOL AMPLIFICATION PRODUCTS CAPILLARY ELECTROPHORESIS, TO SEPARATE AMPLIFICATION PRODUCTS BY SIZE
DETECT UNIQUELY-SIZED AMPLIFICATION PRODUCTS CONTAINING PRIMERS 1-25, 26-50, 52-76, 77-101, AMPLIFICATION PRODUCT CONTAINING PRIMER 51 MISSING BECAUSE TEST COMPOUND ACTED ON CORRESPONDING GENE PRODUCT

FIG. 2B

FIG. 3

FIG. 3A
FIG. 3B

FIG. 3A

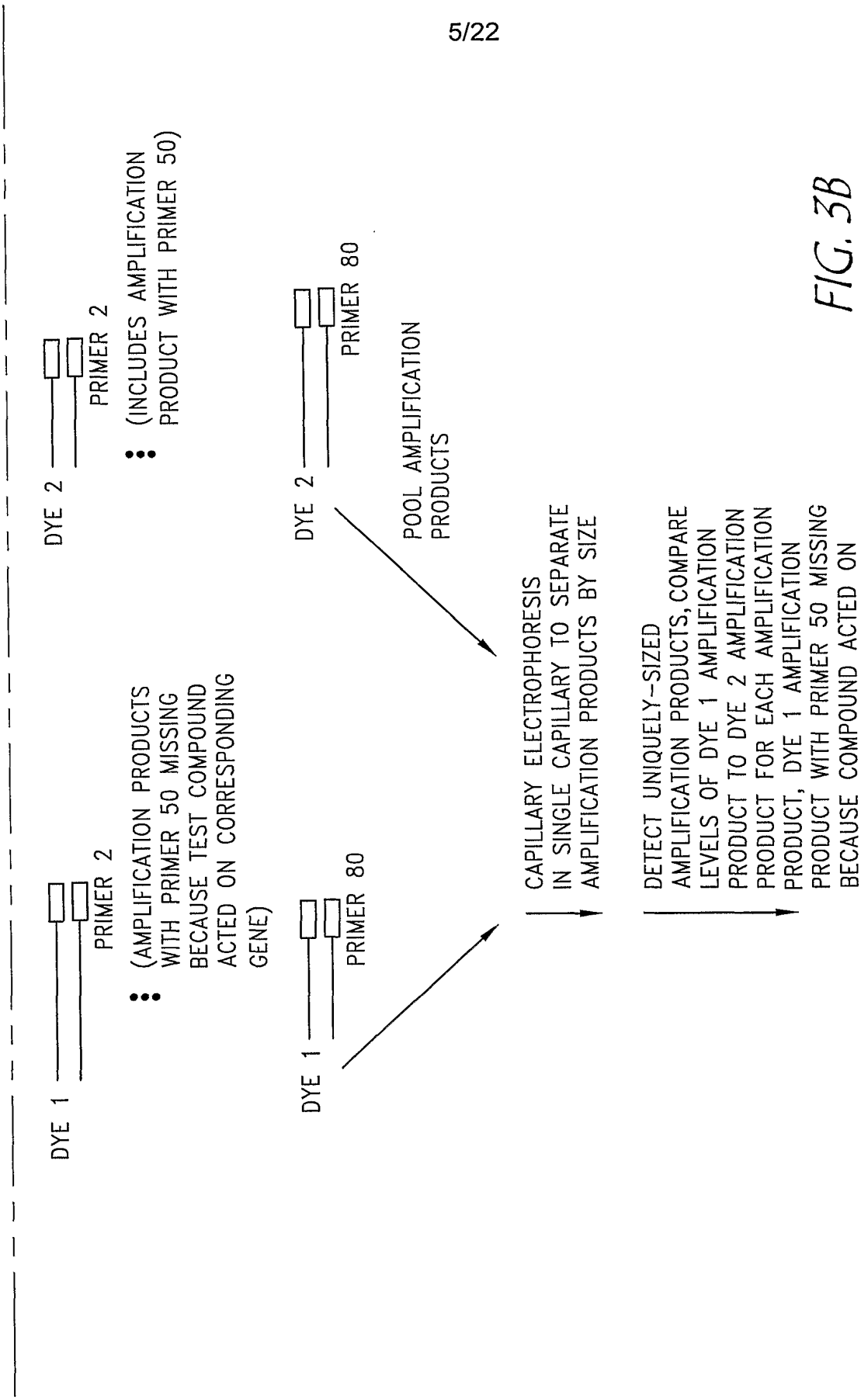

DYE 1
PRIMER 2
(AMPLIFICATION PRODUCTS WITH PRIMER 50 MISSING BECAUSE TEST COMPOUND ACTED ON CORRESPONDING GENE)
DYE 2
PRIMER 2
(INCLUDES AMPLIFICATION PRODUCT WITH PRIMER 50)
DYE 1
PRIMER 80
DYE 2
PRIMER 80
POOL AMPLIFICATION PRODUCTS
CAPILLARY ELECTROPHORESIS IN SINGLE CAPILLARY TO SEPARATE AMPLIFICATION PRODUCTS BY SIZE
DETECT UNIQUELY-SIZED AMPLIFICATION PRODUCTS, COMPARE LEVELS OF DYE 1 AMPLIFICATION PRODUCT TO DYE 2 AMPLIFICATION PRODUCT FOR EACH AMPLIFICATION PRODUCT, DYE 1 AMPLIFICATION PRODUCT WITH PRIMER 50 MISSING BECAUSE COMPOUND ACTED ON CORRESPONDING GENE PRODUCT, DYE 2 AMPLIFICATION PRODUCT WITH PRIMER 50 IS PRESENT

FIG. 3B

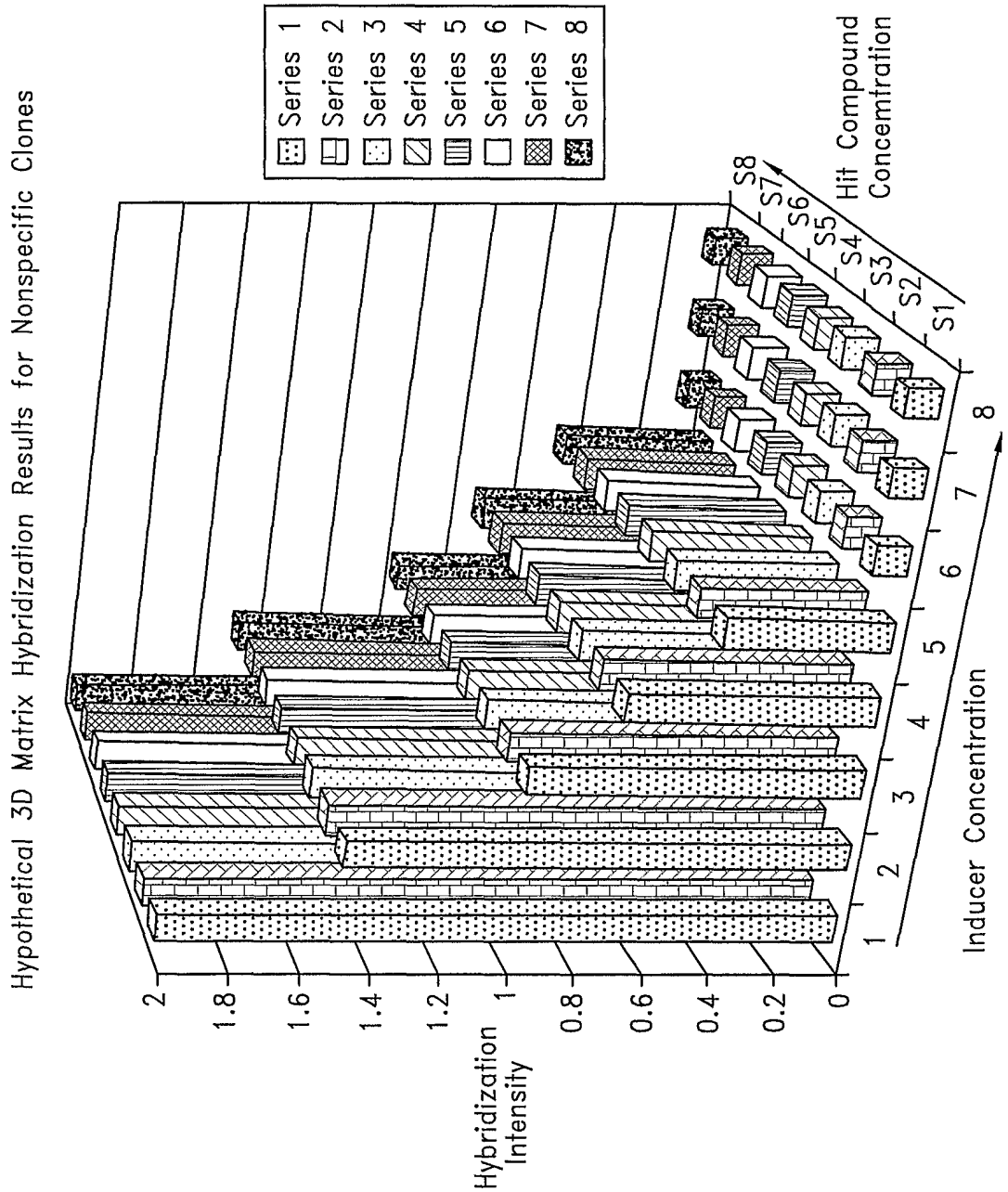

Hypothetical 3D Matrix Hybridization Results for Nonspecific Clones
Series 1
Series 2
Series 3
Series 4
Series 5
Series 6
Series 7
Series 8
Hybridization Intensity
0
0.2
0.4
0.6
0.8
1
1.2
1.4
1.6
1.8
2
Inducer Concentration
1
2
3
4
5
6
7
8
Hit Compound Concemtration
S1
S2
S3
S4
S5
S6
S7
S8

FIG. 4

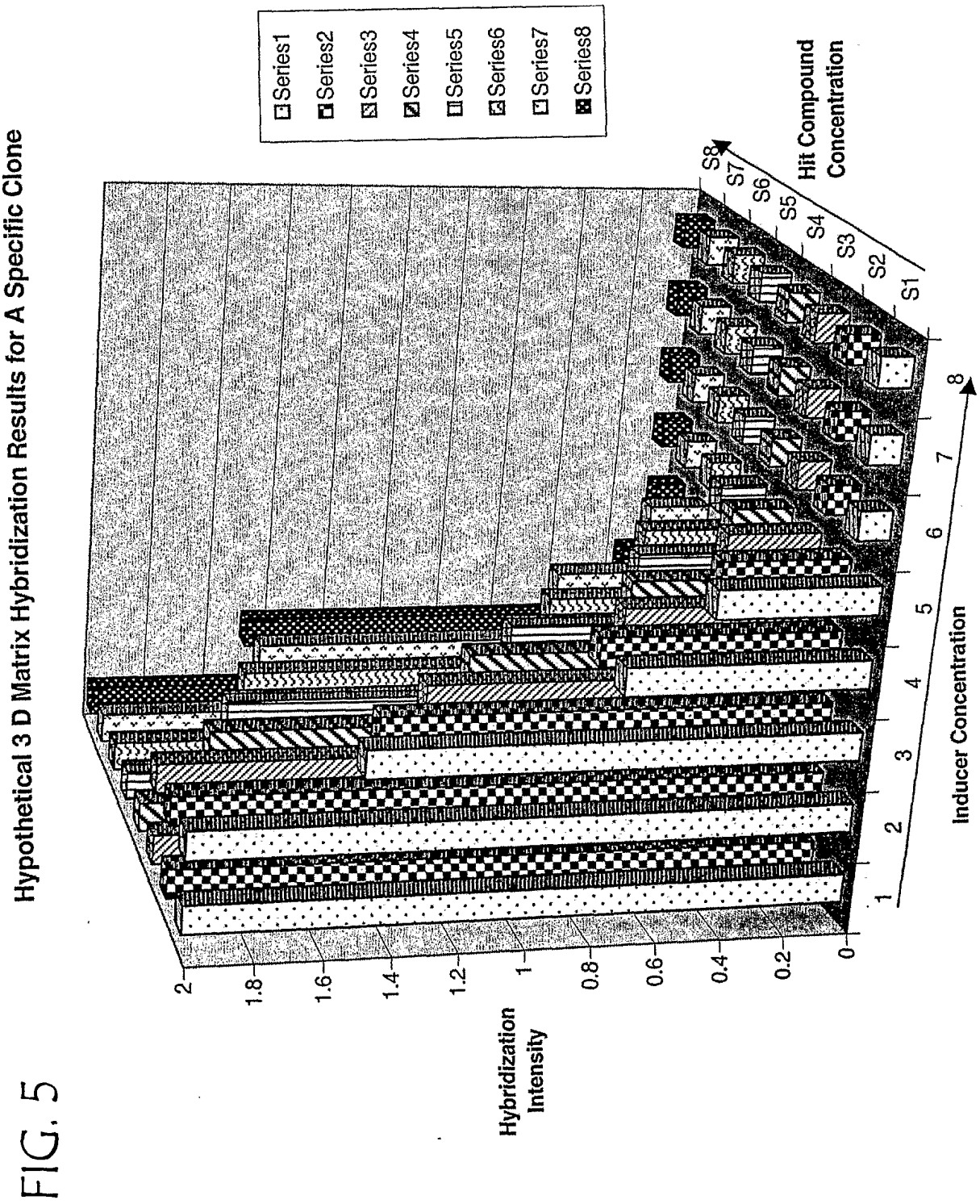
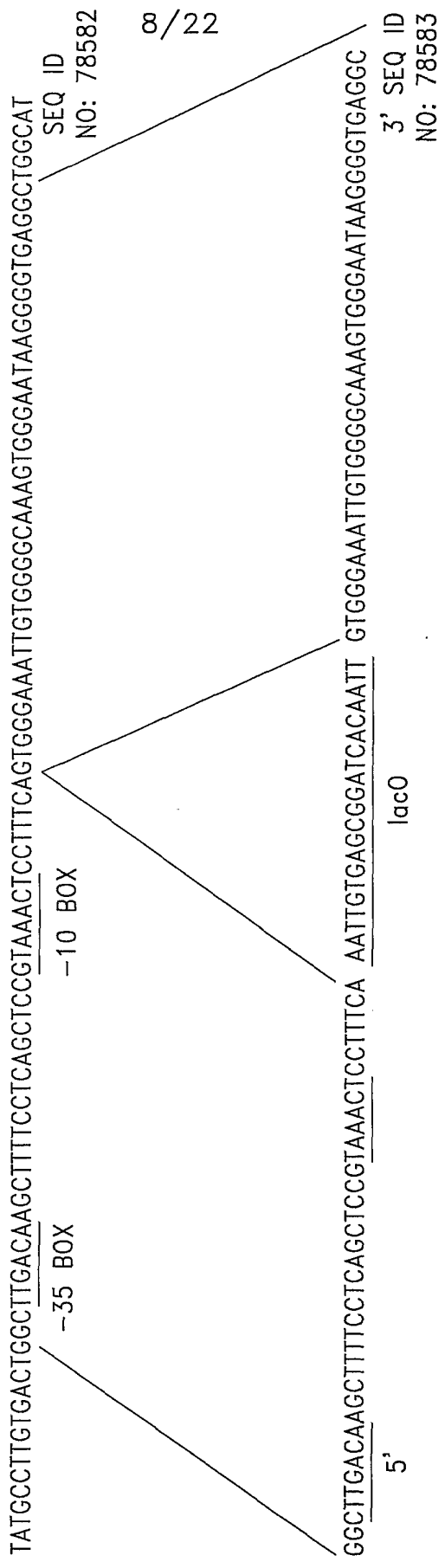

Hypothetical 3 D Matrix Hybridization Results for A Specific Clone
Series1
Series2
Series3
Series4
Series5
Series6
Series7
Series8
Hit Compound Concentration
S8
S7
S6
S5
S4
S3
S2
S1
Inducer Concentration
1
2
3
4
5
6
7
8
Hybridization Intensity
0
0.2
0.4
0.6
0.8
1
1.2
1.4
1.6
1.8
2

FIG. 5

FIG. 6


PROMOTER FOR yabB yabC ftsL ftsI murE OPERON
TATGCCTTGTGACTGGCTTGACAAGCTTTTCCTCAGCTCCGTAAACTCCTTTCAGTGGGAAATTGTGGGGCAAAGTGGGAATAAGGGGTGAGGCTGGCAT
SEQ ID NO: 78582
-35 BOX
-10 BOX
5'
GGCTTGACAAGCTTTTCCTCAGCTCCGTAAACTCCTTTCA AATTGTGAGCGGATCACAATT GTGGGAAATTGTGGGGCAAAGTGGGAATAAGGGGTGAGGC
3' SEQ ID NO: 78583
lacO
OLIGO USED FOR lacO INSERTION

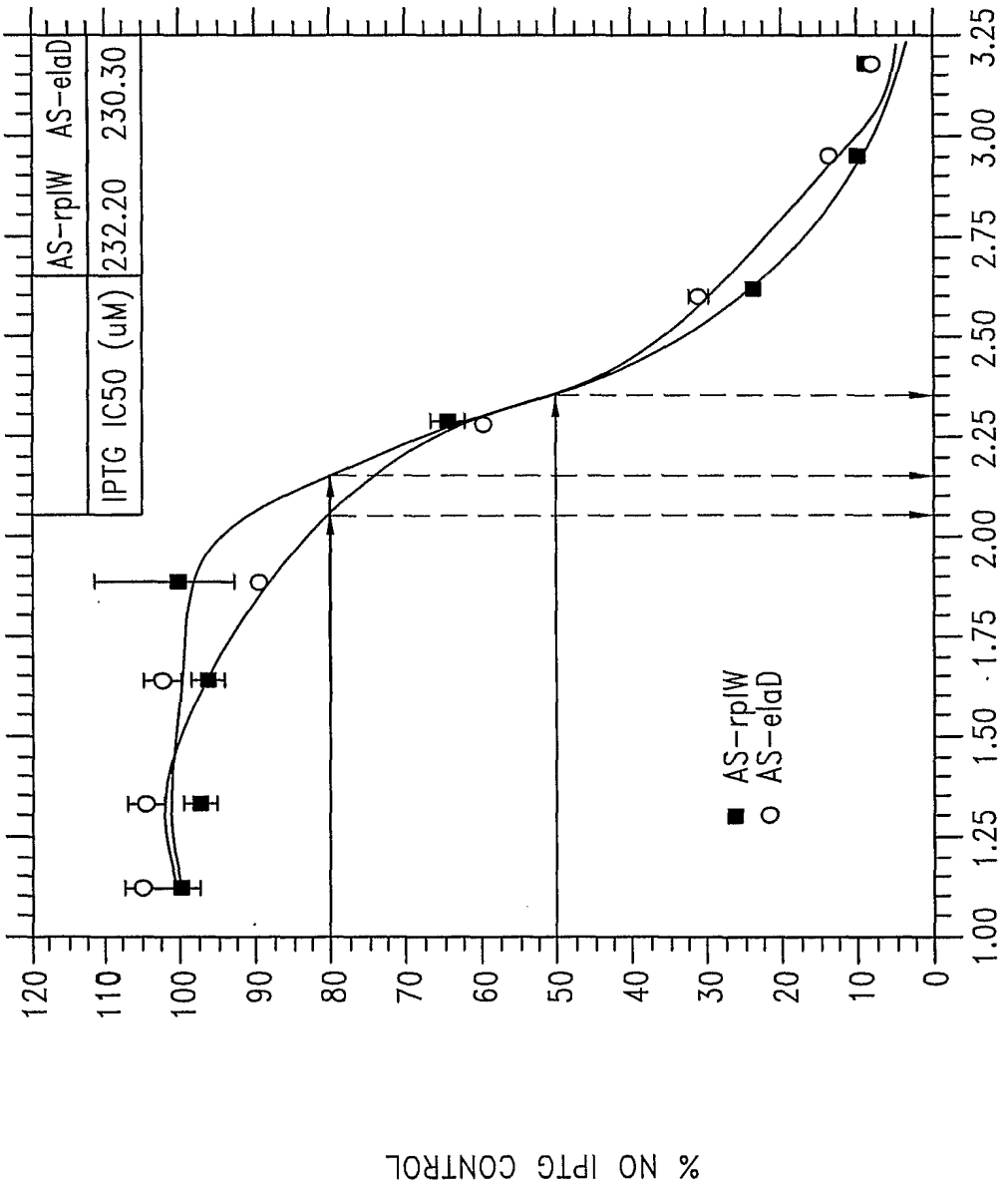

AS-rplW AS-elaD
IPTG IC50 (uM) 232.20 230.30
AS-rplW
AS-elaD
% NO IPTG CONTROL
LOG (uM IPTG)
120
110
100
90
80
70
60
50
40
30
20
10
0
1.00
1.25
1.50
1.75
2.00
2.25
2.50
2.75
3.00
3.25

FIG. 7

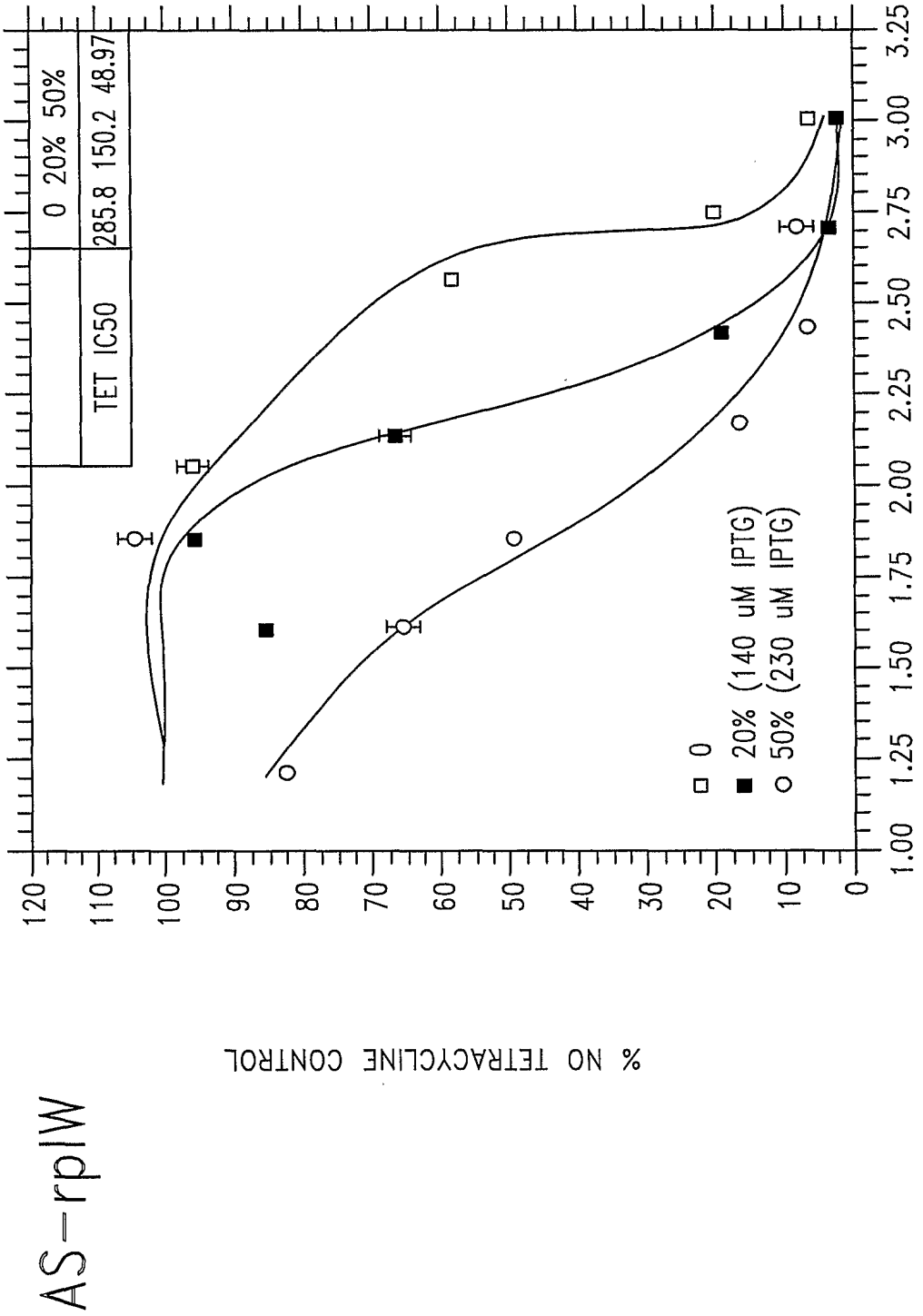

AS-rpIW
% NO TETRACYCLINE CONTROL
LOG (ng/ml TETRACYCLINE)
TET IC50
0 20% 50%
285.8 150.2 48.97
0
20% (140 uM IPTG)
50% (230 uM IPTG)

FIG. 8A

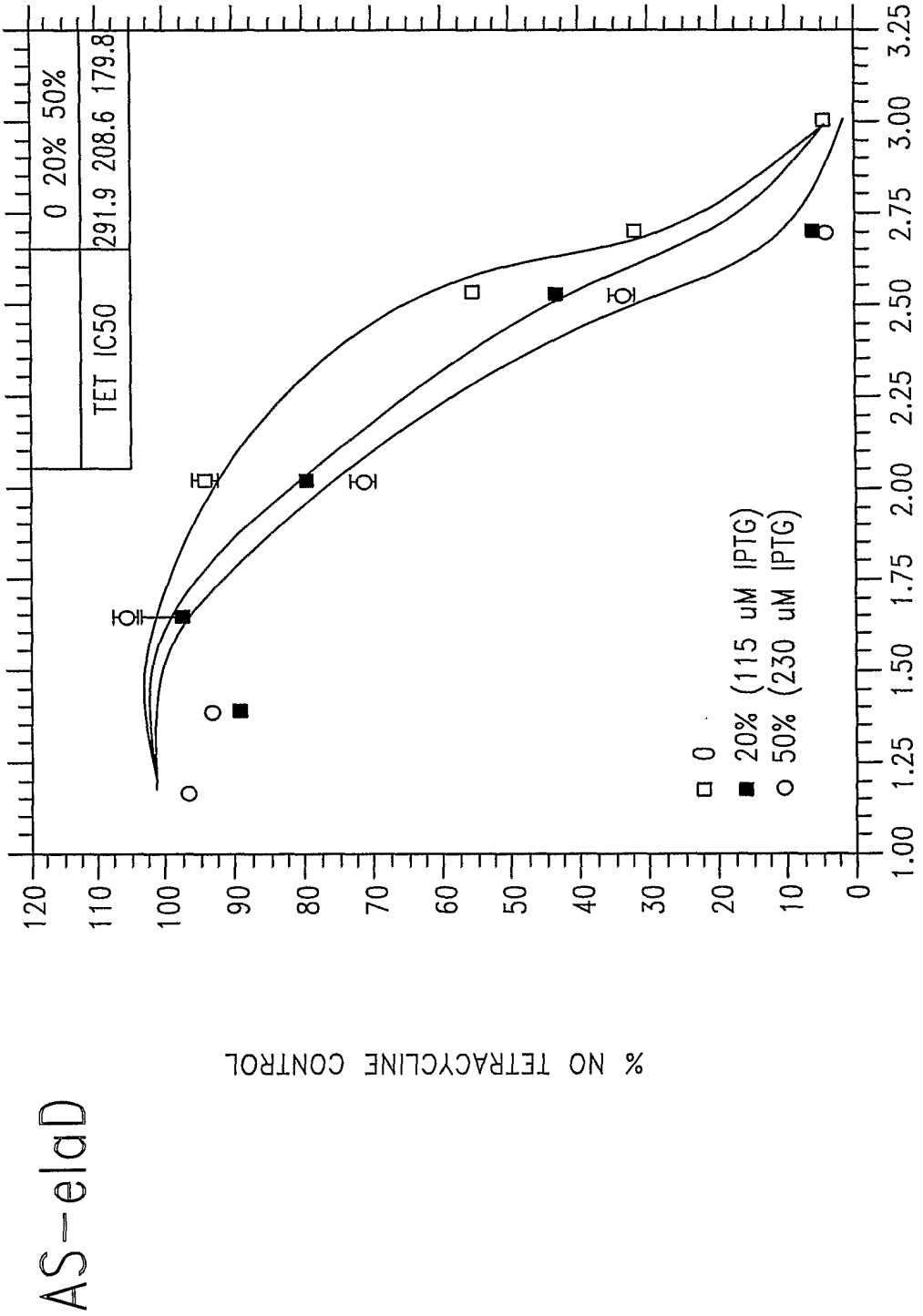

AS-eladD
% NO TETRACYCLINE CONTROL
LOG (ng/ml TETRACYCLINE)
TET IC50
0 20% 50%
291.9 208.6 179.8
0
20% (115 uM IPTG)
50% (230 uM IPTG)

FIG. 8B

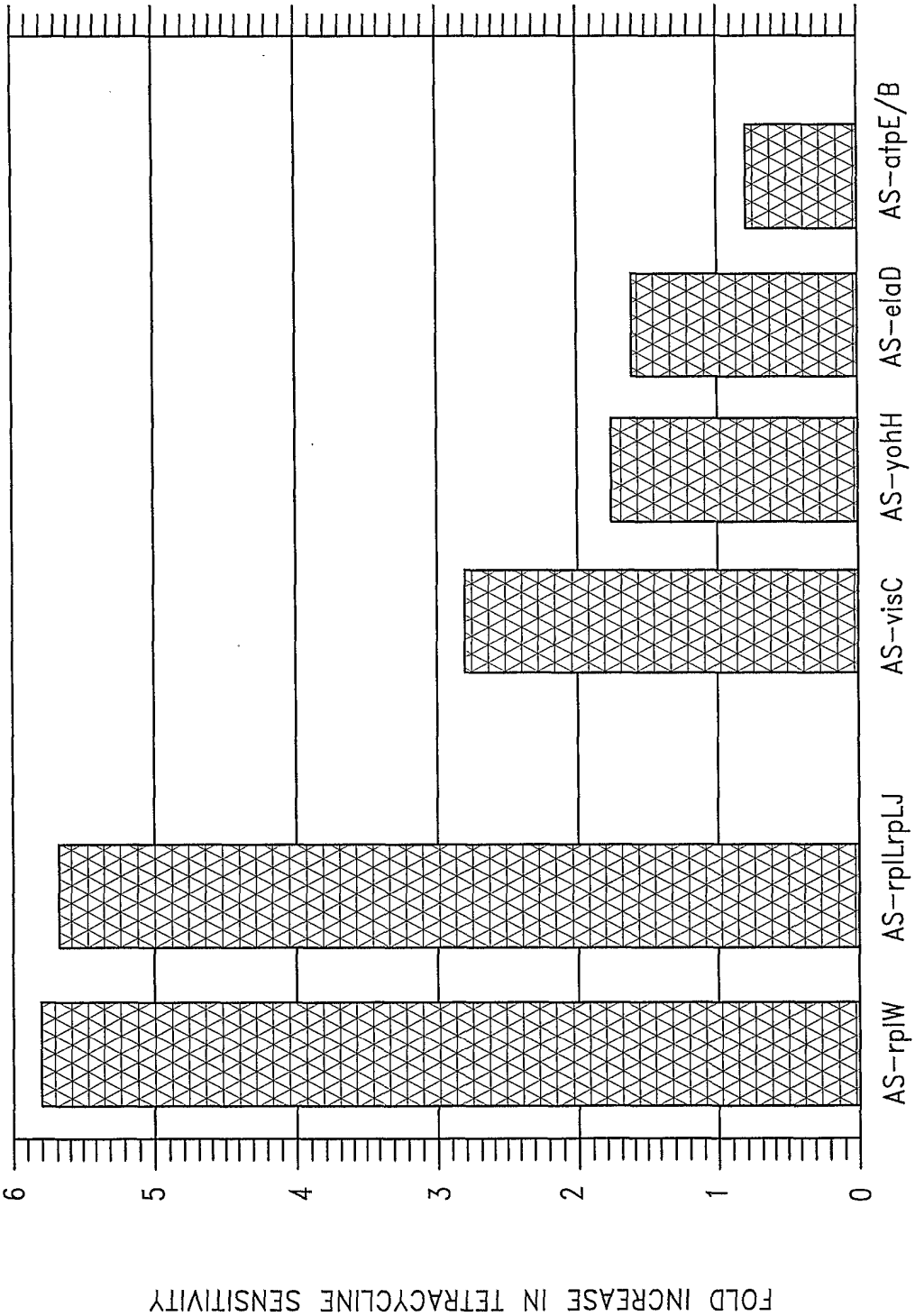

AS-rplW
AS-rplLrpLJ
AS-visC
AS-yohH
AS-elaD
AS-atpE/B
0
1
2
3
4
5
6
FOLD INCREASE IN TETRACYCLINE SENSITIVITY

FIG. 9

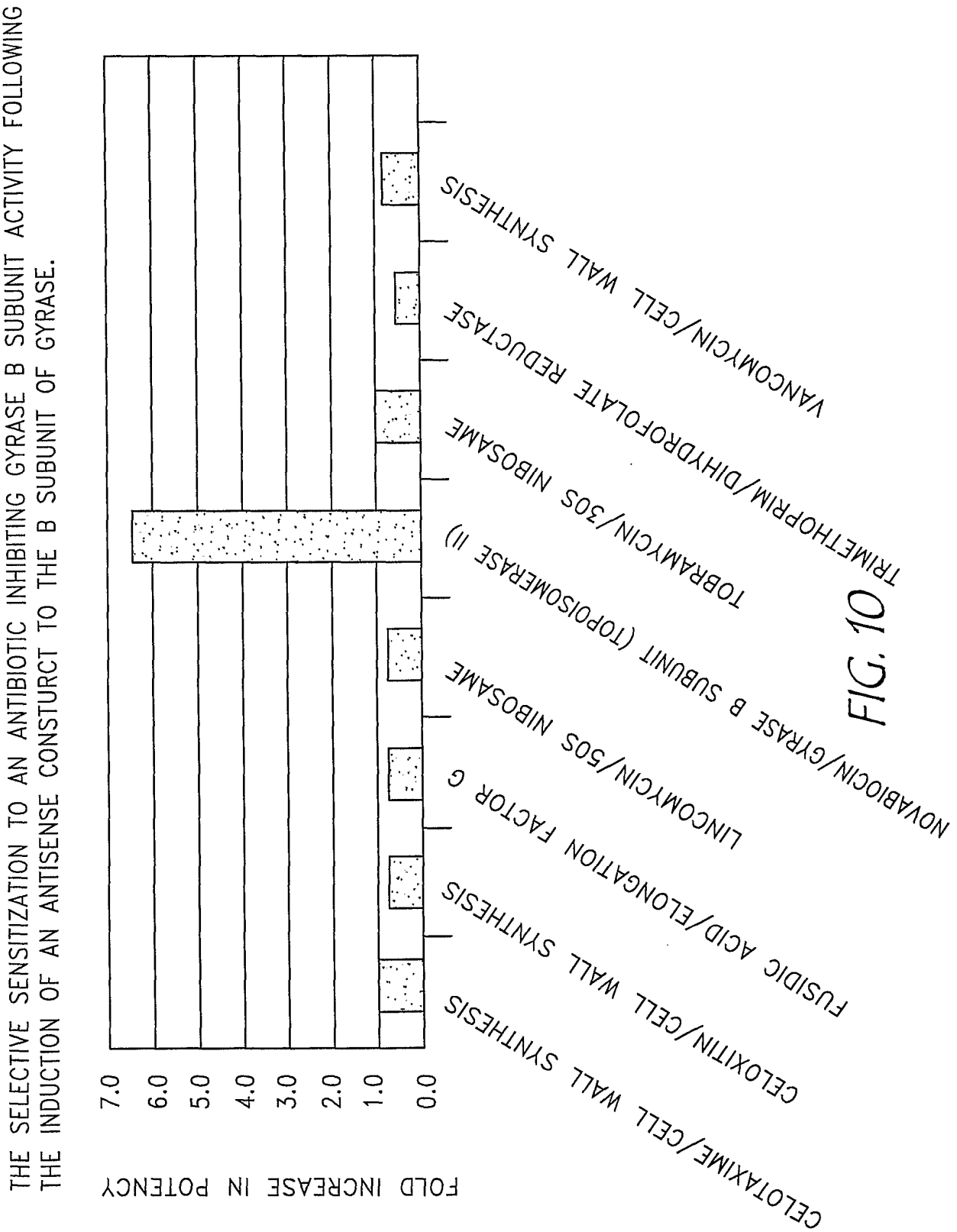
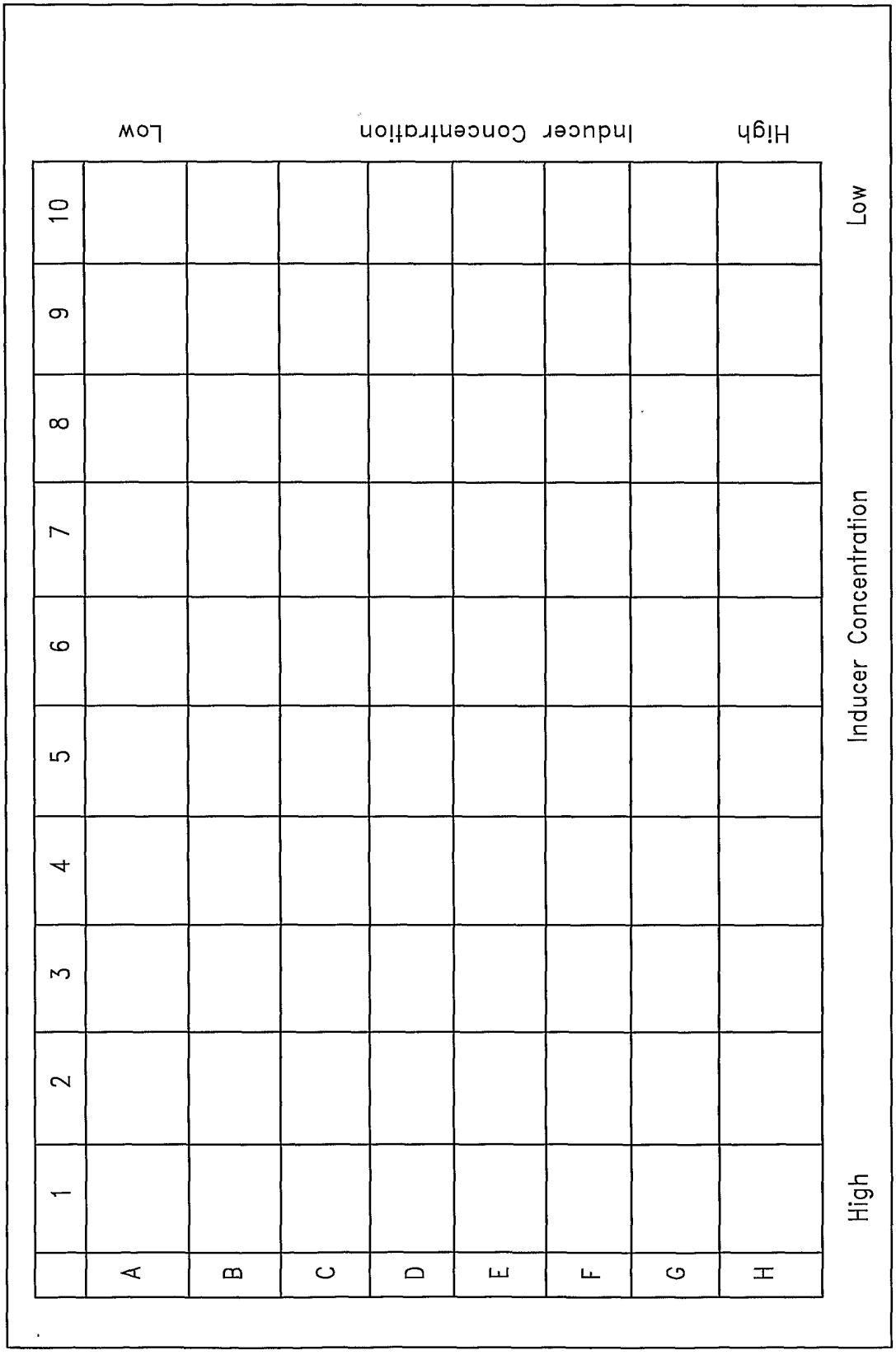

THE SELECTIVE SENSITIZATION TO AN ANTIBIOTIC INHIBITING GYRASE B SUBUNIT ACTIVITY FOLLOWING THE INDUCTION OF AN ANTISENSE CONSTURCT TO THE B SUBUNIT OF GYRASE.
FOLD INCREASE IN POTENCY
7.0
6.0
5.0
4.0
3.0
2.0
1.0
0.0
CELOTAXIME/CELL WALL SYNTHESIS
CELOXITIN/CELL WALL SYNTHESIS
FUSIDIC ACID/ELONGATION FACTOR G
LINCOMYCIN/50S NIBOSAME
NOVABIOCIN/GYRASE B SUBUNIT (TOPOISOMERASE II)
TOBRAMYCIN/30S NIBOSAME
TRIMETHOPRIM/DIHYDROFOLATE REDUCTASE
VANCOMYCIN/CELL WALL SYNTHESIS

FIG. 10

FIG. 11


Inducer Concentration
High
Low
Inducer Concentration
High
Low
1
2
3
4
5
6
7
8
9
10
A
B
C
D
E
F
G
H

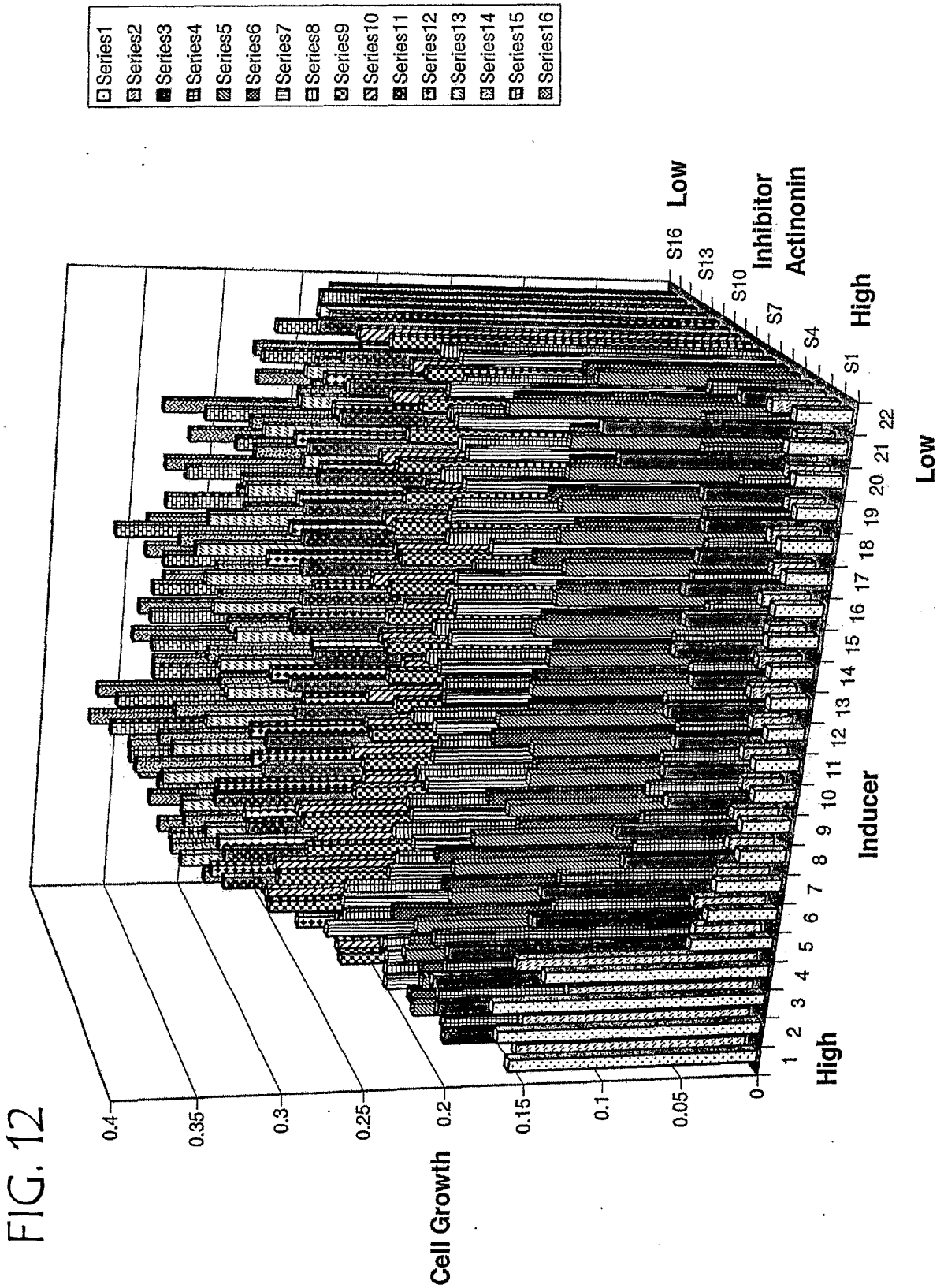

Series1
Series2
Series3
Series4
Series5
Series6
Series7
Series8
Series9
Series10
Series11
Series12
Series13
Series14
Series15
Series16
Cell Growth
0.4
0.35
0.3
0.25
0.2
0.15
0.1
0.05
0
High
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22
Low
Inducer
S16 Low
S13
S10
S7 Inhibitor
S4 Actinonin
S1 High

FIG. 12

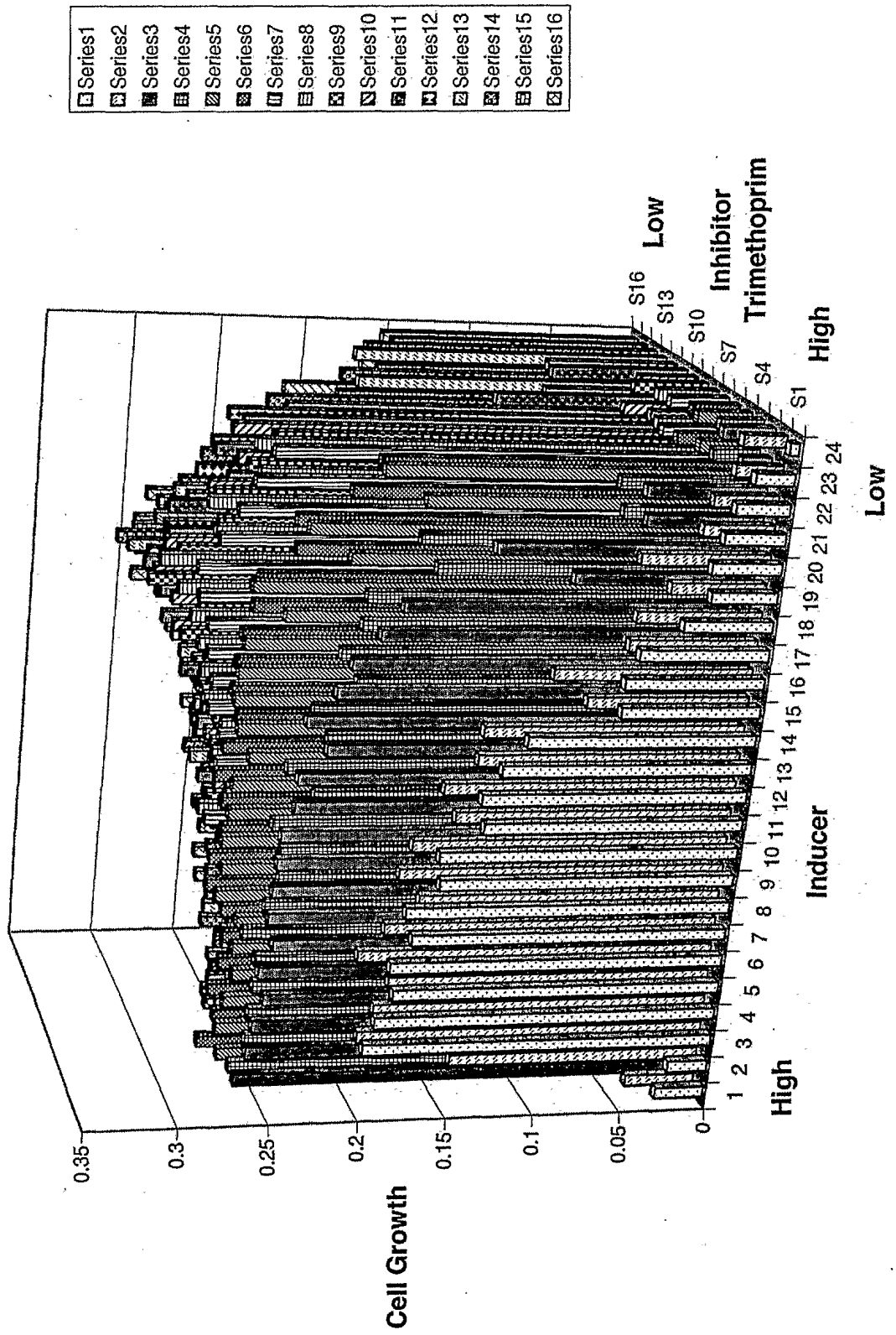

Series1
Series2
Series3
Series4
Series5
Series6
Series7
Series8
Series9
Series10
Series11
Series12
Series13
Series14
Series15
Series16
Cell Growth
0.35
0.3
0.25
0.2
0.15
0.1
0.05
0
High
Inducer
Low
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24
High
Trimethoprim
Inhibitor
Low
S1
S4
S7
S10
S13
S16

FIG. 13

FIG. 14

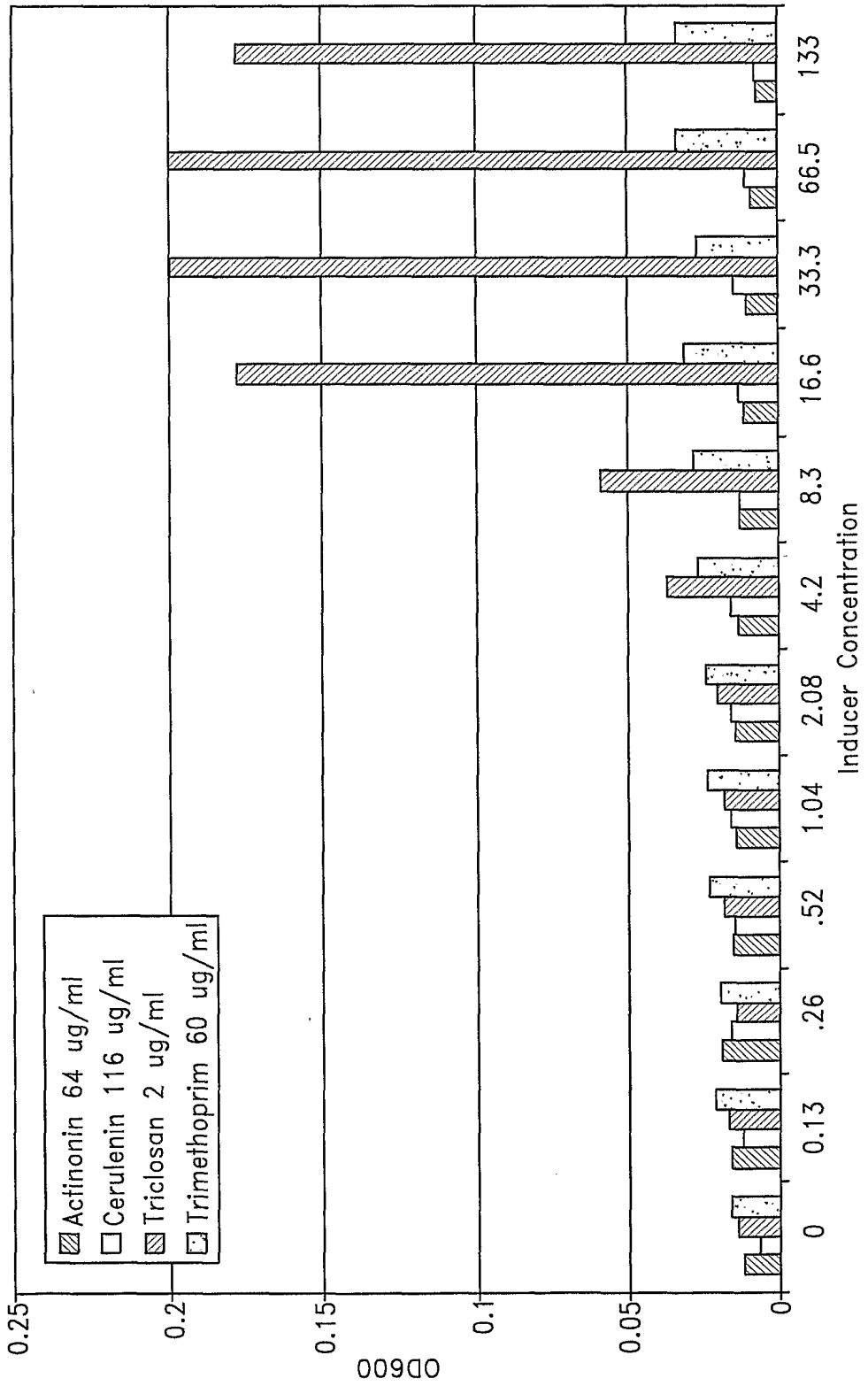

Actinonin 64 ug/ml
Cerulenin 116 ug/ml
Triclosan 2 ug/ml
Trimethoprim 60 ug/ml
OD600
0.25
0.2
0.15
0.1
0.05
0
0
0.13
.26
.52
1.04
2.08
4.2
8.3
16.6
33.3
66.5
133
Inducer Concentration

FIG. 15

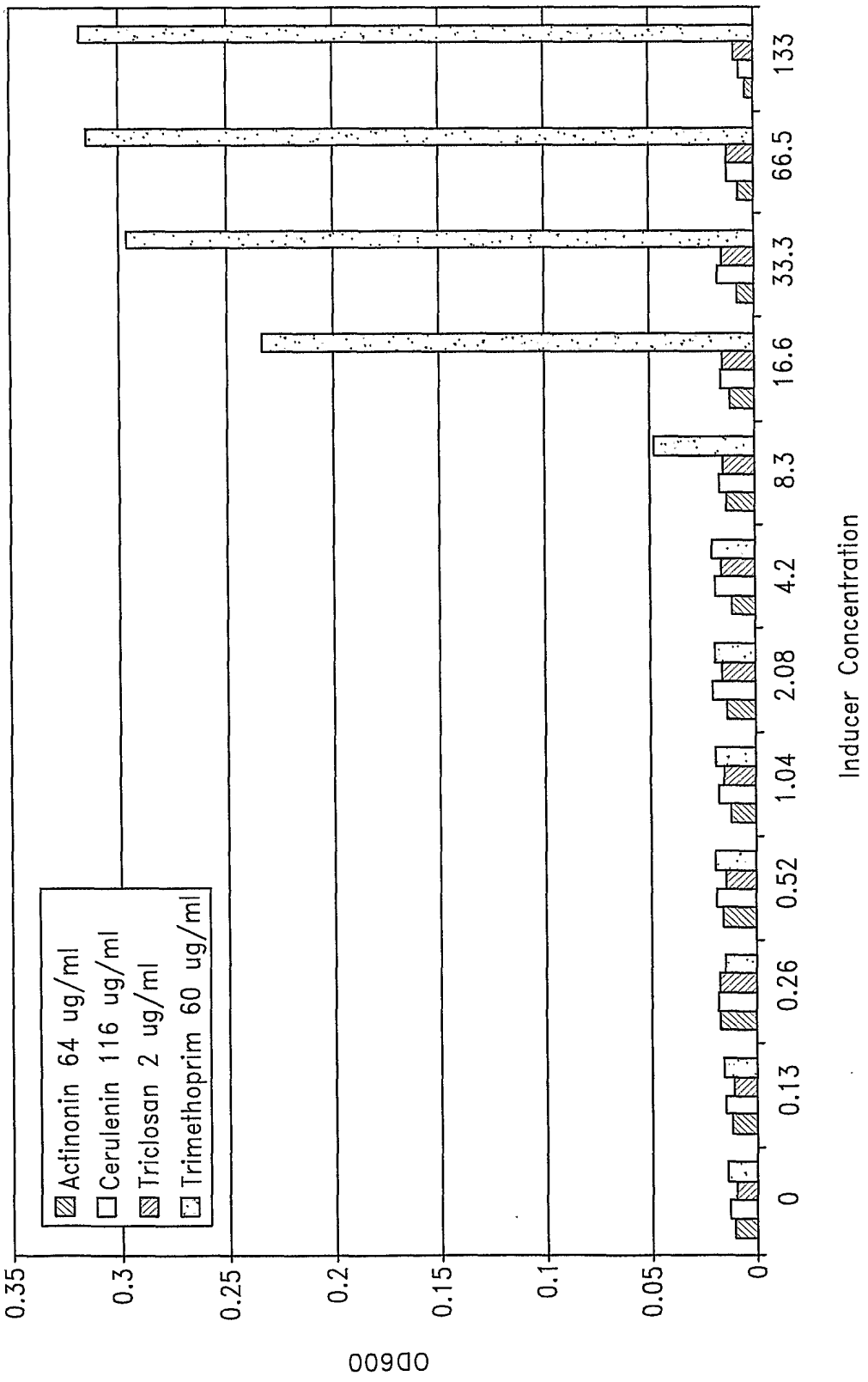

OD600
0.35
0.3
0.25
0.2
0.15
0.1
0.05
0
Actinonin 64 ug/ml
Cerulenin 116 ug/ml
Triclosan 2 ug/ml
Trimethoprim 60 ug/ml
0
0.13
0.26
0.52
1.04
2.08
4.2
8.3
16.6
33.3
66.5
133
Inducer Concentration

FIG. 16

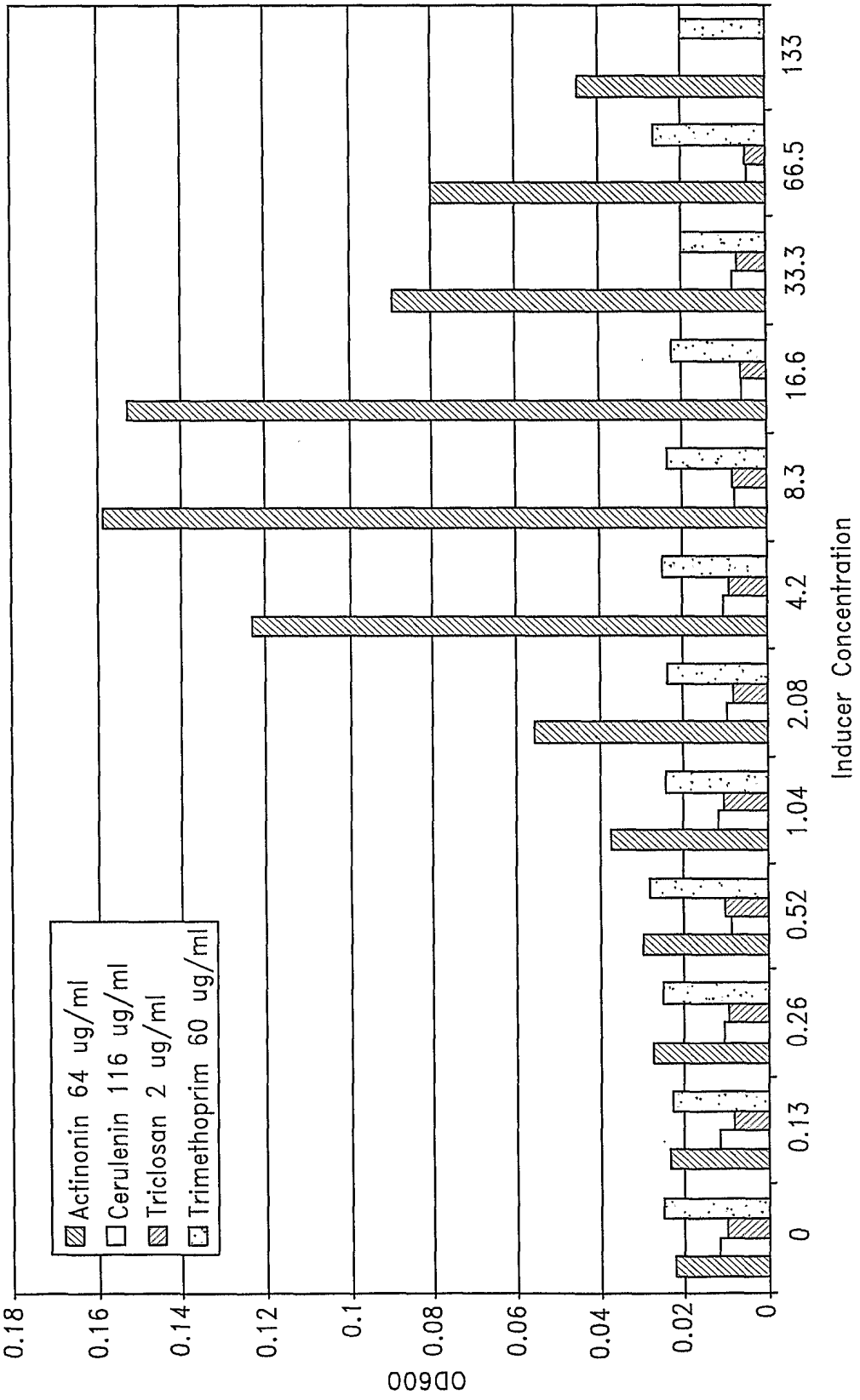

Actinonin 64 ug/ml
Cerulenin 116 ug/ml
Triclosan 2 ug/ml
Trimethoprim 60 ug/ml
OD600
0.18
0.16
0.14
0.12
0.1
0.08
0.06
0.04
0.02
0
0
0.13
0.26
0.52
1.04
2.08
4.2
8.3
16.6
33.3
66.5
133
Inducer Concentration

FIG. 17

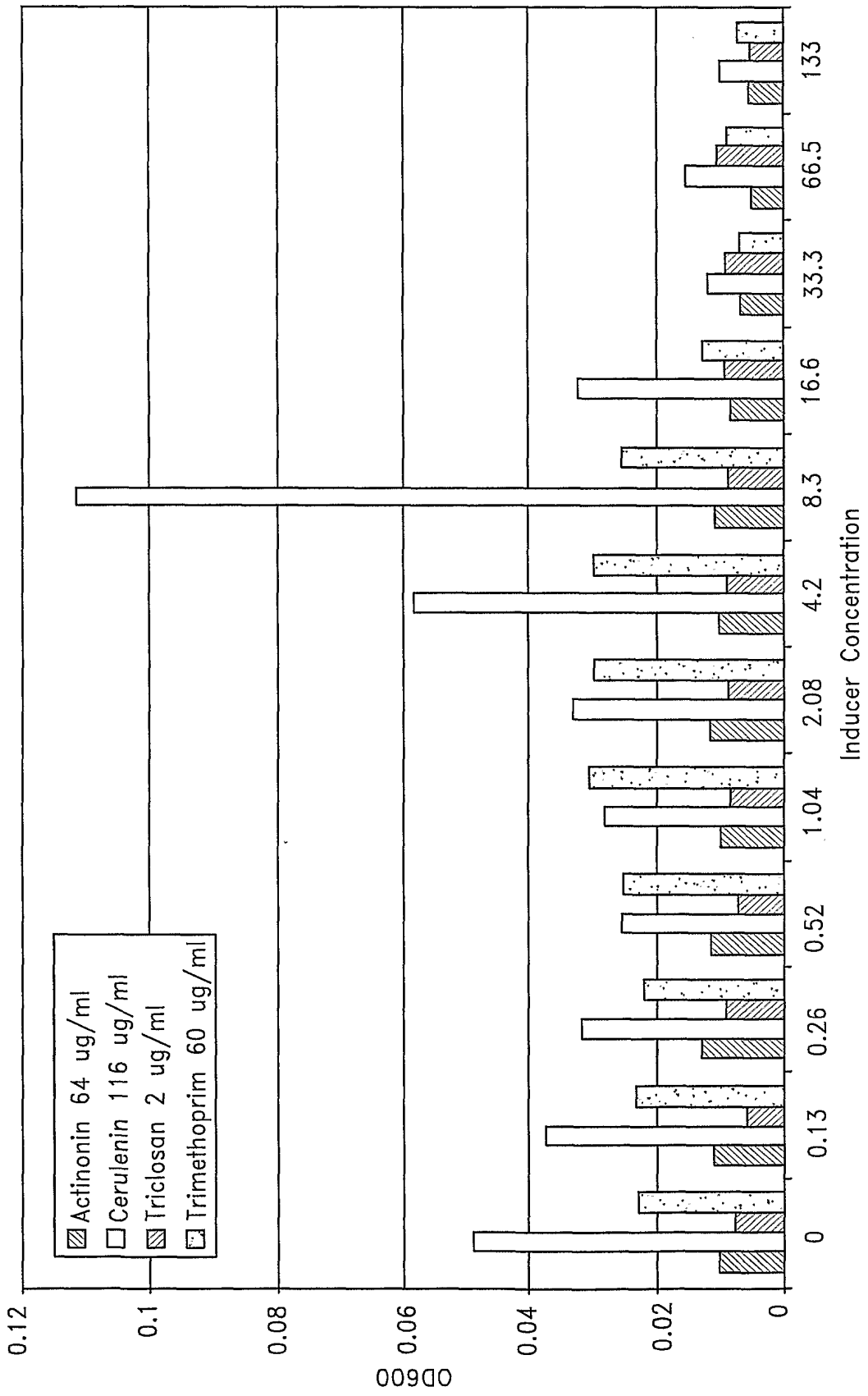

Actinonin 64 ug/ml
Cerulenin 116 ug/ml
Triclosan 2 ug/ml
Trimethoprim 60 ug/ml
OD600
0.12
0.1
0.08
0.06
0.04
0.02
0
0
0.13
0.26
0.52
1.04
2.08
4.2
8.3
16.6
33.3
66.5
133
Inducer Concentration

FIG. 18

FIG. 18A

FIG. 18B

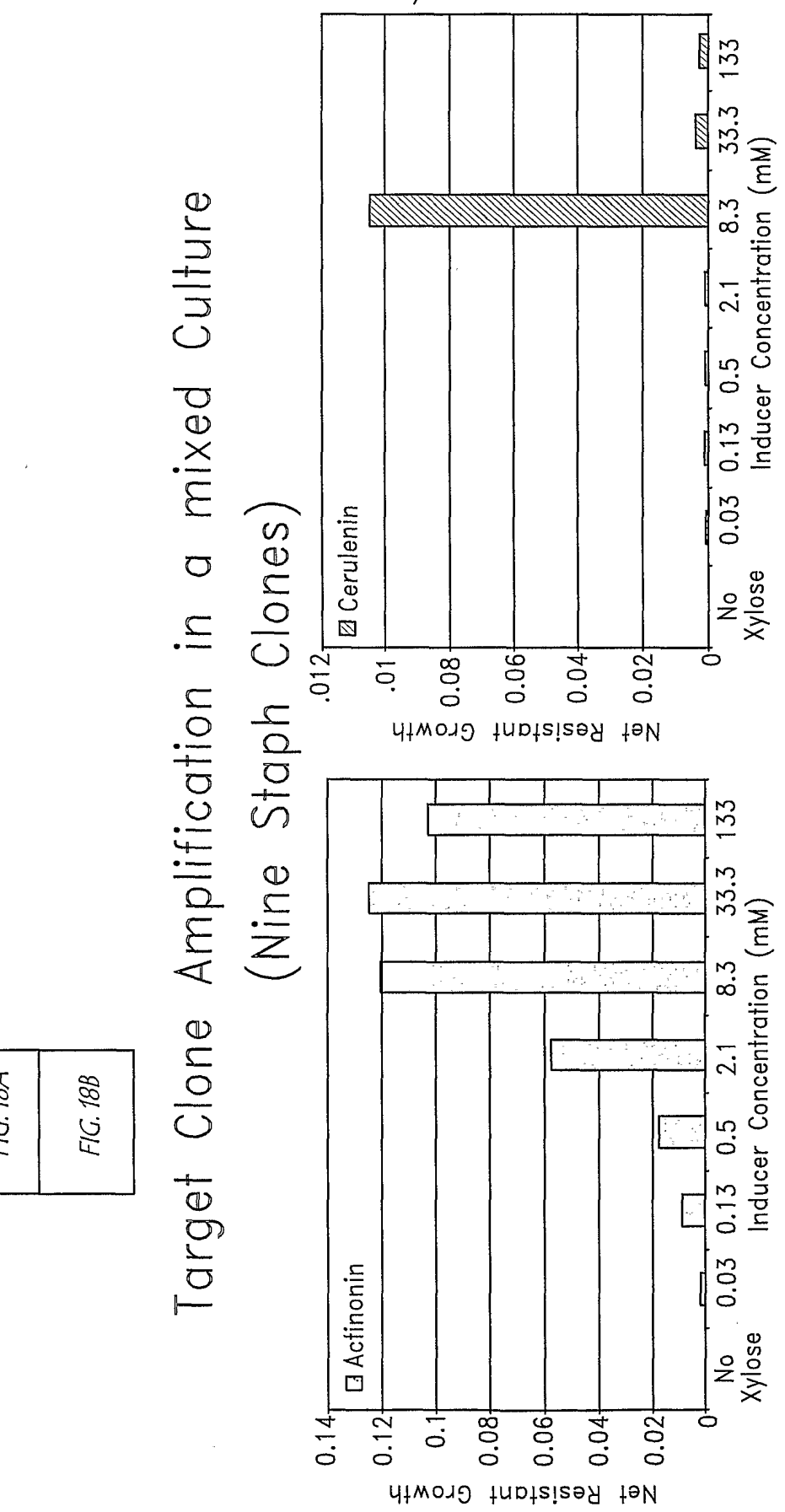


FIG. 18

FIG. 18A
FIG. 18B

FIG. 18B